

From: Minnifield, Nita
Sent: Thursday, June 09, 2005 11:36 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

CRFE

STIC

09/970076

Please do a commercial and interference sequence search on the following sequences of the above application.

Please search sequences against aa and nt databases.

SEQ ID NO: 1, nt 104-1207 of SEQ ID NO: 1 - 1414 NP

SEQ ID NO: 2, aa 27-321 of SEQ ID NO: 2 - 308 AA
aa 28-320 of SEQ ID NO: 2
aa 41-227 of SEQ ID NO: 2
aa 44-216 of SEQ ID NO: 2
aa 42-222 of SEQ ID NO: 2

Please provide a paper copy of all results.

Thanks,
Minnifield
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

_____ Other CLN

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 22, 2004, 01:18:40 ; Search time 47.4808 Seconds

(without alignments)
2547.963 Million cell updates/sec

Title: US-09-970-076-10

Perfect score: 1131
Sequence: 1 MSFVFSRGTGTTMKLTEDR.....STSGKKGNSHPCLPAPHT 218

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Fgapop 10.0 , Fgapext 0.5	
Dgapop 6.0 , Dgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFMT=fastcap -SUFFIX=rxn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=binom62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
1: /cg2_6/ptodata/2/lna/5A.COMB.seq:*
2: /cg2_6/ptodata/2/lna/5B.COMB.seq:*
3: /cg2_6/ptodata/2/lna/6A.COMB.seq:*
4: /cg2_6/ptodata/2/lna/6B.COMB.seq:*
5: /cg2_6/ptodata/2/lna/ECTUS.COMB.seq:*
6: /cg2_6/ptodata/2/lna/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1131	100.0	1609	4	US-09-620-312D-8 Sequence 8, Appl
2	966	85.4	2459	4	US-09-833-381-998 Sequence 998, App
3	128.5	11.4	3519	1	US-08-286-889-45 Sequence 45, Appl
4	128.5	11.4	3519	1	US-08-485-618-45 Sequence 45, Appl
5	128.5	11.4	3519	1	US-08-362-652-45 Sequence 45, Appl
6	128.5	11.4	3519	1	US-08-605-672-45 Sequence 45, Appl
7	128.5	11.4	3519	2	US-08-482-293A-45 Sequence 45, Appl
8	128.5	11.4	3519	2	US-08-943-363-45 Sequence 45, Appl
9	128.5	11.4	3519	3	US-09-193-043-45 Sequence 45, Appl
10	128.5	11.4	3519	4	US-09-688-307A-45 Sequence 45, Appl
11	128.5	11.4	3519	4	US-09-350-259-45 Sequence 45, Appl
12	128.5	11.4	3803	1	US-08-485-618-52 Sequence 52, Appl

13	128.5	11.4	3803	1	US-08-362-652-52	Sequence 52, Appl
14	128.5	11.4	3803	1	US-08-605-672-52	Sequence 52, Appl
15	128.5	11.4	3803	2	US-08-482-293A-52	Sequence 52, Appl
16	128.5	11.4	3803	2	US-08-943-363-52	Sequence 52, Appl
17	128.5	11.4	3803	3	US-09-193-043-52	Sequence 52, Appl
18	128.5	11.4	3803	4	US-09-688-307A-52	Sequence 52, Appl
19	128.5	11.4	3803	4	US-09-350-259-52	Sequence 52, Appl
20	122	10.8	3528	1	US-08-286-889-36	Sequence 36, Appl
21	122	10.8	3528	1	US-08-485-618-36	Sequence 36, Appl
22	122	10.8	3528	1	US-08-362-652-36	Sequence 36, Appl
23	122	10.8	3528	1	US-08-605-672-36	Sequence 36, Appl
24	122	10.8	3528	2	US-08-482-293A-36	Sequence 36, Appl
25	122	10.8	3528	2	US-08-943-363-36	Sequence 36, Appl
26	122	10.8	3528	3	US-09-193-043-36	Sequence 36, Appl
27	122	10.8	3528	4	US-09-688-307A-36	Sequence 36, Appl
28	122	10.8	3528	4	US-09-350-259-36	Sequence 36, Appl
29	122	10.8	3597	1	US-08-485-618-54	Sequence 54, Appl
30	122	10.8	3597	1	US-08-362-652-54	Sequence 54, Appl
31	122	10.8	3597	1	US-08-605-672-54	Sequence 54, Appl
32	122	10.8	3597	2	US-08-482-293A-54	Sequence 54, Appl
33	122	10.8	3597	2	US-08-943-363-54	Sequence 54, Appl
34	122	10.8	3597	3	US-09-193-043-54	Sequence 54, Appl
35	122	10.8	3597	4	US-09-688-307A-54	Sequence 54, Appl
36	122	10.8	3597	4	US-09-350-259-54	Sequence 54, Appl
37	114	10.1	2499	1	US-08-485-618-96	Sequence 96, Appl
38	114	10.1	2499	1	US-08-605-672-96	Sequence 96, Appl
39	114	10.1	2499	2	US-08-482-293A-96	Sequence 96, Appl
40	114	10.1	2499	2	US-08-943-363-96	Sequence 96, Appl
41	114	10.1	2499	3	US-09-193-043-96	Sequence 96, Appl
42	114	10.1	2499	4	US-09-688-307A-96	Sequence 96, Appl
43	114	10.1	2499	4	US-09-350-259-96	Sequence 96, Appl
44	114	10.1	3726	1	US-08-173-497-1	Sequence 1, Appl
45	114	10.1	3726	1	US-08-286-889-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-620-312D-8
Sequence 8, Application US/09620312D
Patent No. 6569662
GENERAL INVENTION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehman, Tom
APPLICANT: Xue, Aiding J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Duntui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 8
LENGTH: 1609
TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.:      8e-148      Length:      1609
Score:          1131.00     Matches:      218
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%     Indels:      0
DB:              4          Gaps:          0

US-09-970-076-10 (1-218) x US-09-620-312D-8 (1-1609)

Qy      1 MetSerPheIleValPheSerThrArgLYThrThrLeuMetIysLeuThrGluAspArg 20
Db      546 ATGTCCTTATTTGTTTCTCCACCCGAGGAACACCTTAATGAACTGACGAAGACAGA 605

Qy      21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnIysValLeuProGlyGlyAspThrTyr 40
Db      606 GAACAAATCCGTCAGAGCCTAGAAAGACTCCAGAAAGTTCTGCCAGAGAGACACTTAC 665

Qy      41 MethIsgIugLYPheGluArgAlaSerGluGlnIleTyrTYrGluAsnArgGlnGlyTyr 60
Db      666 ATGCATGAAGATTGAAAGGGCCAGTGAGCAGATTATTATGAAACAGACAAAGGCTAC 725

Qy      61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisIsgIuAspLeuPhePhe 80
Db      726 AGGACAGCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCCAGAAAGATCTCTTTTC 785

Qy      81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyValIleValIleTyrCysValGly 100
Db      786 TATTCAGAGAGGAGGAGCTTAATAGCTCTGAGATCTTGTCATTTGTTACTGTGTGCT 845

Qy      101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLYAspHisValPhe 120
Db      846 GTGAAAGATTCAATGAGACACAGCTGGCCGGATTGGGACAGTAAGATCATGTGTTT 905

Qy      121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysSer 140
Db      906 CCCGTAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAGGCC 965

Qy      141 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
Db      966 TGCATCGAAATTTCTAGACGCTGAAACCATCCACATATGTGACGAGAGCTATTTCAAGTT 1025

Qy      161 ValValaArgGlyAsnGlyPheArgHisAlaArgAsnValaAspArgValLeuCysSerPhe 180
Db      1026 GTCGTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGCAAGCTTC 1085

Qy      181 LysIleAsnAspSerValThrLeuSerIysSerLeuGlnSerProTTPValSerSerThr 200
Db      1086 AAGATCAATGACTCGCTCACACTCAGTAAGTCTTGACAGAGTCCATGGGTTTCTTCGCA 1145

Qy      201 SerGlyPheLYsGluGlyAsnSerHisProCysLeuProAlaArgProHisThr 218
Db      1146 AGTGGCTTCAGAGAGGAAATTCACCTTGTCTTCACGACAGGCCACACACA 1199

RESULT 2
US-09-833-381-998
; Sequence 998, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; PRIORITY FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIORITY FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 2050
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; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 998
; LENGTH: 2459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2459)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-998

Alignment Scores:
Pred. No.:      2.01e-124     Length:      2459
Score:          966.00       Matches:      188
Percent Similarity: 100.00%   Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match:    85.41%       Indels:      0
DB:              4          Gaps:          0

US-09-970-076-10 (1-218) x US-09-833-381-998 (1-2459)

Qy      1 MetSerPheIleValPheSerThrArgLYThrThrLeuMetIysLeuThrGluAspArg 20
Db      649 ATGTCCTTATTTGTTTCTCCACCCGAGGAACAACTTAATGAACTGACGAAGACAGA 708

Qy      21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnIysValLeuProGlyGlyAspThrTyr 40
Db      709 GAACAAATCCGTCAGAGCCTAGAAAGACTCCAGAAAGTTCTGCCAGAGAGACACTTAC 768

Qy      41 MethIsgIugLYPheGluArgAlaSerGluGlnIleTyrTYrGluAsnArgGlnGlyTyr 60
Db      769 ATGCATGAAGATTGAAAGGGCCAGTGAGCAGATTATTATGAAACAGACAAAGGCTAC 828

Qy      61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisIsgIuAspLeuPhePhe 80
Db      829 AGGACAGCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCCAGAAAGATCTCTTTTC 888

Qy      81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyValIleValIleTyrCysValGly 100
Db      889 TATTCAGAGAGGAGGAGCTTAATAGCTCTGAGATCTTGTCATTTGTTACTGTGTGCT 948

Qy      101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLYAspHisValPhe 120
Db      949 GTGAAAGATTCAATGAGACACAGCTGGCCGGATTGCGGACAGTAAGATCATGTGTTT 1008

Qy      121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysSer 140
Db      1009 CCCGTAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAGTCC 1068

Qy      141 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
Db      1069 TGCATCGAAATTTCTAGACGCTGAAACCATCCACATATGTGACGAGAGCTATTTCAAGTT 1128

Qy      161 ValValaArgGlyAsnGlyPheArgHisAlaArgAsnValaAspArgValLeuCysSerPhe 180
Db      1129 GTCGTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGCAAGCTTC 1188

Qy      181 LysIleAsnAspSerValThrLeuSerIys 190
Db      1189 AAGATCAATGACTCGTGCACATCAATGAG 1218

RESULT 3
US-08-286-889-45
; Sequence 45, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; FILE REFERENCE: Van der Vlieten, Monica
; CURRENT APPLICATION NUMBER: No. 5470953el Human 2 Integrin Alpha Subunit
; PRIORITY FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIORITY FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 2050
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
```


Qy 12 ThrluWetlyLeuThrluAspArgGluGlnIleArgGlnIleuGluGln 31
Db 664 ACGGAATTCAAGAGAGAGCTGAGCCCTGAGAGCTGGTGAATGCATCTCACTCAA 723
Qy 32 LysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGln 51
Db 724 -----GGCTGACGACACAGCTCGGAGATCCAGAAAGTGTAAGAG 768
Qy 52 IleTyrTyrGluAsnArgGlnIleTyrArgThrAla---SerValIleIleAlaLeuThr 70
Db 769 CTATTCTTACCAAGAAATGGGAGCCGAAAGATGCCCAAGAAAGATATTGTCTATCA 828
Qy 71 AspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsnArg 88
Db 829 GATGGGCAAGAAATTCAGAGACCCCTGAGATATGACATGATCATCCCTGAAGAGAGAA 888
Qy 89 SerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu--- 106
Db 889 GCT-----GGGATCATTCGCTATCTATAGGGGTGGAGATGCTTCGAGAAACC 939
Qy 107 ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhePro 121
Db 940 ACTGCCCTTACAGAGAGCTGAACACCATTTGGCTCAGCTCCCTCGAGAGACCATGTTCAAG 999
Qy 122 ValAsnAspGlyPheGlnAlaLeuGlnIleIleHisSerIleLeuLysSerCys 141
Db 1000 GTGGGCAAT---TTTGTAGCACTTCGAGCATCCAGCGCAAAATTCAGAGAAA----- 1050
Qy 142 IleGluIleLeuAlaGluProSerThrIleCysValGlyGluSerPheGlnValVal 161
Db 1051 -----ATCTTGTGCATTGAAGAACCGAATCAAGGTCAAGTTCCTTTCAGACAGAG 1104
Qy 162 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 174
Db 1105 ATGTCAAGAAAGTTTCACTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 5
US-08-362-652-45
Sequence 45, Application US/08362652
Parent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-362-652-45

Alignment Scores:
Pred. No.: 5,9e-07 Length: 3519
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69
Query Match: 11.36% Indels: 23
Gaps: 9

US-09-970-076-10 (1-218) x US-08-362-652-45 (1-3519)

Qy 12 ThrluWetlyLeuThrluAspArgGluGlnIleArgGlnIleuGluGln 31
Db 664 ACGGAATTCAAGAGAGAGCTGAGCCCTGAGAGCTGGTGAATGCATCTCACTCAA 723
Qy 32 LysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGln 51
Db 724 -----GGCTGACGACACAGCTCGGAGATCCAGAAAGTGTAAGAG 768
Qy 52 IleTyrTyrGluAsnArgGlnIleTyrArgThrAla---SerValIleIleAlaLeuThr 70
Db 769 CTATTCTTACCAAGAAATGGGAGCCGAAAGATGCCCAAGAAAGATATTGTCTATCA 828
Qy 71 AspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsnArg 88
Db 829 GATGGGCAAGAAATTCAGAGACCCCTGAGATATGACATGATCATCCCTGAAGAGAGAA 888
Qy 89 SerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu--- 106
Db 889 GCT-----GGGATCATTCGCTATCTATAGGGGTGGAGATGCTTCGAGAAACC 939
Qy 107 ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhePro 121
Db 940 ACTGCCCTTACAGAGAGCTGAACACCATTTGGCTCAGCTCCCTCGAGAGACCATGTTCAAG 999
Qy 122 ValAsnAspGlyPheGlnAlaLeuGlnIleIleHisSerIleLeuLysSerCys 141
Db 1000 GTGGGCAAT---TTTGTAGCACTTCGAGCATCCAGCGCAAAATTCAGAGAAA----- 1050
Qy 142 IleGluIleLeuAlaGluProSerThrIleCysValGlyGluSerPheGlnValVal 161
Db 1051 -----ATCTTGTGCATTGAAGAACCGAATCAAGGTCAAGTTCCTTTCAGACAGAG 1104
Qy 162 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 174
Db 1105 ATGTCAAGAAAGTTTCACTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 6
US-08-605-672-45
Sequence 45, Application US/08605672
Parent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago

```

STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-605-672-45

Alignment Scores:
Pred. No.: 5.9e-07 Length: 3519
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69
Query Match: 11.36% Indels: 23
DB: 1 Gaps: 9

US-09-970-076-10 (1-218) x US-08-605-672-45 (1-3519)
QY 12 ThrleuMetLysLeuThrGluValArgGlnGlnIleArgGlnIleLeuGlnIleLeuGln 31
DB 664 ACCGAAATTCAGAGAGAGCCCTGAGAGCCCTGAGAGCCCTGAGAGCCCTGAGAGCCCTGAGAG 723
QY 32 LysValLeuProGlyGlyLysThrGlyMetGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 51
DB 724 -----GGCCTGAGTACAGAGAGCCCTGAGAGCCCTGAGAGCCCTGAGAGCCCTGAGAG 768
QY 52 IleTyrGlnLysValArgGlnIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 70
DB 769 CATTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 828
QY 71 ArgGlnLysLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 88
DB 829 GATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 888
QY 89 SerArgLysLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 106
DB 889 GCT-----GGATCATTCGCTATGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939
QY 107 ThrGlnLeuAlaArgIle-----AlaSerSerLysAspHisValPhePro 121

```

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DB 940 ACTGCCCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
QY 122 ValAsnArgGlyPheGlnAlaLeuGlnGlnIleIleHisSerIleLeuLysSerGys 141
DB 1000 GTGGGCAAT---TTGTAGACCTTCGAGCATCCAGCCGCAAAATTCAGAGAGAA----- 1050
QY 142 IleGlnIleLeuAlaGlnProSerThrIleCysAlaGlnGlnGlnGlnGlnGlnGlnGln 161
DB 1051 -----ATCTTGGCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1104
QY 162 ValArgGlnLysLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 174
DB 1105 ATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1143

RESULT 7
US-08-482-293A-45
Sequence 45, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 233 South Wacker Drive, 6300 Seair Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-482-293A-45

Alignment Scores:
Pred. No.: 5.9e-07 Length: 3519
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69

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Query Match: 11.36% Indels: 23
DB: 2 Gaps: 9
US-09-970-076-10 (1-218) x US-08-482-293A-45 (1-3519)
Qy 12 ThrleuMetLyleuThrgluAerArgluGluGlnGlyleuGluGluGln 31
Db 664 ACCGAATTCAAGAGAGCCCTGAGCCCTGAGAGATGCGATGCTGAGTCCAA 723
Qy 32 LysValleuProGlyLysArgThrMetHisGluGlyPheGluArgAlaSerGluGln 51
Db 724 -----GGCTGACGTACACAGCCCTGGGCAATCCGAAGGTGTGAAGAG 768
Qy 52 IleTyrTyrGluAerArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeuThr 70
Db 769 CTATTTCATACAGAAATGGGGCCCGAAGAGTGCAGAAATATGTCATCA 828
Qy 71 AspGlyGluLeuHisGluAerLeuPhePheTyrSerGlu-----ArgGluAlaAerArg 88
Db 829 GATGGCGCAAAATTCAGAGACCCCTGGAGTATAGACATGTCATCCCTGAAGCAGAGAA 888
Qy 89 SerArgAerLeuGlyAlaIleValTyrCysValGlyValLysAer---PheAerGlu--- 106
Db 889 GCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCGGGAACCC 939
Qy 107 ThrGluLeuAlaArgIle-----AlaAerSerLysAerPheValPhePro 121
Db 940 ACTGCCCTACAGAGAGTGAACCATGCTGCTGAGCTCCCTGCGAGACCATGTTCAAG 999
Qy 122 ValAerAerGlyPheGluAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 141
Db 1000 GTGGGCAT---TTTGTAGCACTTCGAGCATCCAGCGCAAAATTCAGAGAAA----- 1050
Qy 142 IleGluIleuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGluValVal 161
Db 1051 -----ATCTTGCCATTGAAAGAACCAATCAAGTCAAGTAGTCTTTTCAGACAGAG 1104
Qy 162 ValArgGlyAerGlyPheArgHisAlaArgAerValAer 174
Db 1105 ATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143
RESULT 8
US-08-943-363-45
Sequence 45, Application US/08943363
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5837478 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943.363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO.: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-943-363-45
Alignment Scores:
Pred. No.: 5.9e-07 Length: 3519
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69
Query Match: 11.36% Indels: 23
DB: 2 Gaps: 9
US-09-970-076-10 (1-218) x US-08-943-363-45 (1-3519)
Qy 12 ThrleuMetLyleuThrgluAerArgluGluGlnGlyleuGluGluGln 31
Db 664 ACCGAATTCAAGAGAGCCCTGAGCCCTGAGAGATGCGATGCTGAGTCCAA 723
Qy 32 LysValleuProGlyLysArgThrMetHisGluGlyPheGluArgAlaSerGluGln 51
Db 724 -----GGCTGACGTACACAGCCCTGGGCAATCCGAAGGTGTGAAGAG 768
Qy 52 IleTyrTyrGluAerArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeuThr 70
Db 769 CTATTTCATACAGAAATGGGGCCCGAAGAGTGCAGAAATATGTCATCA 828
Qy 71 AspGlyGluLeuHisGluAerLeuPhePheTyrSerGlu-----ArgGluAlaAerArg 88
Db 829 GATGGCGCAAAATTCAGAGACCCCTGGAGTATAGACATGTCATCCCTGAAGCAGAGAA 888
Qy 89 SerArgAerLeuGlyAlaIleValTyrCysValGlyValLysAer---PheAerGlu--- 106
Db 889 GCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCGGGAACCC 939
Qy 107 ThrGluLeuAlaArgIle-----AlaAerSerLysAerPheValPhePro 121
Db 940 ACTGCCCTACAGAGAGTGAACCATGCTGCTGAGCTCCCTGCGAGACCATGTTCAAG 999
Qy 122 ValAerAerGlyPheGluAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 141
Db 1000 GTGGGCAT---TTTGTAGCACTTCGAGCATCCAGCGCAAAATTCAGAGAAA----- 1050
Qy 142 IleGluIleuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGluValVal 161
Db 1051 -----ATCTTGCCATTGAAAGAACCAATCAAGTCAAGTAGTCTTTTCAGACAGAG 1104
Qy 162 ValArgGlyAerGlyPheArgHisAlaArgAerValAer 174
Db 1105 ATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143
RESULT 9
US-09-193-043-45
Sequence 45, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:

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; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 651395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-193-043-45

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Alignment Scores:
Pred. No.: 5,9e-07 Length: 3519
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69
Query Match: 11.36% Indels: 23
DB: Gaps: 9

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US-09-970-076-10 (1-218) x US-09-193-043-45 (1-3519)
QY 12 ThrleuMeTlyLeuThnGluAspArgGluGlnIleArgGlnGlyLeuGluGluGln 31
DB 664 ACGGAATTCAAGACAGCAGCTGAGCCCTCAGAGCCTGGTGATGCCATGCTCCAGCA 723
QY 32 LysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGln 51
DB 724 -----GGCTGACGTACACAGCCTGGGATCCAGAAAGTGTTGAAGAG 768
QY 52 IleTyrTyrGluAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeuThr 70
DB 769 CTAATTCATACAGCAAGATGGGCGCCGAAAGAGTCCAGAAAGATCTAATGTCATCACA 828
QY 71 AspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsnArg 88
DB 829 GATGGGCAAGAAATTACAGAGACCCCTGAGATATACATGTCATCCCTGAAGCAGAGAA 888
QY 89 SerArgAspLeuGlyAlaIleValTyrCysValGlyValIleAsp---PheAsnGlu--- 106
DB 889 GCT-----GGATCATTCGCTATGCTATAGGGGTGGAGATGCCCTCCGGAGAACCC 939
QY 107 ThrGlnLeuAlaArgIle-----AlaAspSerIleAspHisValAlaPhePro 121
DB 940 ACTGCCCTACAGAGACTGAACACCATGGCTCAGCTCCCTCGCAGAGACACAGTGTCAAG 999
QY 122 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 141
DB 1000 GTGGGCAAT---TTTGTAGCACTTCGACGATCCAGCGCAAAATTCCAGAGAAA----- 1050
QY 142 IleGluIleLeuAlaGluProSerThrIleCysAlaGlyGlySerPheGlnValVal 161
DB 1051 -----ATCTTGGCATTTGAAGAAACCAATCAAGTCAAGTAGTCTTTTACAGACAGAG 1104
QY 162 ValArgGlyAsnGlyPheArgHisAlaAspAsnValAsp 174
DB 1105 ATGTCAAGAAAGATTTCAGCTCAGCTCTCTCAATGAT 1143

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RESULT 10
US-09-688-307A-45
; Sequence 45, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

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Alignment Scores:
Pred. No.: 5,9e-07 Length: 3519
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69
Query Match: 11.36% Indels: 23
DB: Gaps: 9

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US-09-970-076-10 (1-218) x US-09-688-307A-45 (1-3519)
QY 12 ThrleuMeTlyLeuThnGluAspArgGluGlnIleArgGlnGlyLeuGluGluGln 31
DB 664 ACGGAATTCAAGACAGCAGCTGAGCCCTCAGAGCCTGGTGATGCCATGCTCCAGCA 723
QY 32 LysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGln 51
DB 724 -----GGCTGACGTACACAGCCTGGGATCCAGAAAGTGTTGAAGAG 768
QY 52 IleTyrTyrGluAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeuThr 70
DB 769 CTAATTCATACAGCAAGATGGGCGCCGAAAGAGTCCAGAAAGATCTAATGTCATCACA 828
QY 71 AspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsnArg 88
DB 829 GATGGGCAAGAAATTACAGAGACCCCTGAGATATACATGTCATCCCTGAAGCAGAGAA 888
QY 89 SerArgAspLeuGlyAlaIleValTyrCysValGlyValIleAsp---PheAsnGlu--- 106
DB 889 GCT-----GGATCATTCGCTATGCTATAGGGGTGGAGATGCCCTCCGGAGAACCC 939
QY 107 ThrGlnLeuAlaArgIle-----AlaAspSerIleAspHisValAlaPhePro 121
DB 940 ACTGCCCTACAGAGACTGAACACCATGGCTCAGCTCCCTCGCAGAGACACAGTGTCAAG 999
QY 122 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 141
DB 1000 GTGGGCAAT---TTTGTAGCACTTCGACGATCCAGCGCAAAATTCCAGAGAAA----- 1050

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Qy 142 IlegluileuAlaIaIuProserThrileCysAlaIyGluSerPheGluValVal 161
Db 1051 -----ATCTTGCCATGAGAGACCGATCAAGTCAAGTCTCTTCAGACAG 1104
Qy 162 ValArgGlyAenglyPheArgHisAlaArgAsnValAsp 174
Db 1105 ATGTCACAGAGAGTTTCAGCTCAGCTCTCTCATGATG 1143

RESULT 11
US-09-350-259-45
Sequence 45, Application US/09350259
Patent No. 6620915
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: NO. 6620915el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350.259
EARLIER FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193.043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173.497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286.889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362.652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943.363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 45
LENGTH: 3519
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (52) .. (3516)
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-45

Alignment Scores:
Pred. No.: 5.9e-07 Length: 3519
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69
Query Match: 11.36% Indels: 23
Gaps: 9

US-09-970-076-10 (1-218) x US-09-350-259-45 (1-3519)

Qy 12 ThrluueuTyleuThrluAspArgGluGlnleAargGlnlyleuGluGluGlu 31
Db 664 ACGGATTCAGAGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAG 723
Qy 32 LyuValLeuProGlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGln 51
Db 724 -----GGCTGACGTCACACACCTCGGACATCCAGAAAGTGCTGAAAGAG 768
Qy 52 TleTyrTyrGluAsnArgGlnlyTyrArgThrAla---SerValIleIleAlaLeuThr 70
Db 769 CTATTTCATGACAGAAATGGGCGCCGAGAAAGTCCAGAAAGATCTATGTCATGCA 828
Qy 71 AargGlyLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsnArg 88
Db 829 GATGGCGAGAAATTCAGAGCCCTGAGATGATGATGATGATGATGATGATGATGATGAT 888
Qy 89 SerArgAspLeuGlyAlaIleValTyrCysValGlyValLyAsp---PheAsnGlu--- 106
Db 889 GCT-----GGGATCATTCGCTATGCTATAGGGGATGAGATGCTTCCGGAGAACCC 939
Qy 107 ThrGluLeuAlaArgIle-----AlaAspSerLyAspHisValPhePro 121

Db 940 ACTGCCCTACAGAGAGTCAACACCATTTGGCTCAGCTCCCTCGACAGACAGTTCACAG 999
Qy 122 ValAsnAspGlyPheGlnAlaIleGlnGlyIleHisSerIleLeuLySerCys 141
Db 1000 GTGGGCAAT---TTTGAGCATTTCCGACATCCAGCGGCAAAATTCAGAGAA----- 1050
Qy 142 IlegluileuAlaIaIuProserThrileCysAlaIyGluSerPheGluValVal 161
Db 1051 -----ATCTTGCCATGAGAGACCGATCAAGTCAAGTCTCTTCAGACAG 1104
Qy 162 ValArgGlyAenglyPheArgHisAlaArgAsnValAsp 174
Db 1105 ATGTCACAGAGAGTTTCAGCTCAGCTCTCTCATGATG 1143

RESULT 12
US-08-485-618-52
Sequence 52, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: NO. 5728533el Human 2 Integerin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485.618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173.497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286.889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362.652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 3803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3486
US-08-485-618-52

Alignment Scores:
Pred. No.: 6.72e-07 Length: 3803
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31

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Best Local Similarity: 28.90%      Mismatches: 69
Query Match: 11.36%      Indels: 23
DB: 1      Gaps: 9
US-09-970-076-10 (1-218) x US-08-485-618-52 (1-3803)

Qy 12 ThrleuMetlyLeuThrclyuAyrpArgInglInleArygIngllyLeuIngluInleuIn 31
Db 613 ACGGAATTCAAGAGAGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAG 672
Qy 32 LysValLeuProGlyGlyAyrPThrTyTwechIsGluGlyPheGluAyrAlaSerGluIn 51
Db 673 -----GGCCTGAGCTACACAGCCCTGGGATGACCAAGAGTGTGAAGAG 717
Qy 52 IleTyTyGluAenAyrGlnGlyTyTargThrAla---SerValIleIleAlaLeuThr 70
Db 718 CTAATTCATACAGCAAGATGGGCGCCGAAAGTGCAGAGAGATCTAATGTCATCACA 777
Qy 71 AyrGlyGluLeuHISgluAyrLeuPhePheTyTyrSerGlu-----ArgGluAlaAenAyr 88
Db 778 GATGGGCAAGAAATTCAGAGAGCCCTGGAGATATAGACATGTCATCCCTGAAAGAGAGAA 837
Qy 89 SerAyrAyrLeuGlyAlaIleValTyTyrCyValGlyValLyAyrP---PheAenGlu--- 106
Db 838 GCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTCCGGGAGACC 888
Qy 107 ThrGlnLeuAlaAyrGlie-----AlaAyrSerLyAyrPheHisValPhePro 121
Db 889 ACTGCCCTACAGAGAGCTGAAACCATGCTGCTCAGCTCCCTCCAGAGACAGCTGTTCAAG 948
Qy 122 ValAenAyrGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLyAyrSerCyS 141
Db 949 GTGGGCAT---TTTGTAGCACTTCGCAAGCATCCAGCGCAATTCAGAGAGAA----- 999
Qy 142 IleGluIleLeuAlaIleGluProSerThrIleCyValGlyGluSerPheGlnVal 161
Db 1000 -----ATCTTGTGCATTTGAAGAACCGAATCAAGTCAAGTATCTTTCCAGACAGAG 1053
Qy 162 ValAyrGlyAenGlyPheAyrGhiAlaAyrAenValAyr 174
Db 1054 ATGTCAAGAGAGTTTCAGCTCAGCTCTCTCAATGAT 1092

RESULT 13
US-08-362-652-52
; Sequence 52, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,652
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3803 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURES:
; NAME/KEY: CDS
; LOCATION: 1..3486
; US-08-362-652-52

Alignment Scores:
Pred. No.: 6.72e-07      Length: 3803
Score: 128.50      Matches: 50
Percent Similarity: 46.82%      Conservative: 31
Best Local Similarity: 28.90%      Mismatches: 69
Query Match: 11.36%      Indels: 23
DB: 1      Gaps: 9

US-09-970-076-10 (1-218) x US-08-362-652-52 (1-3803)

Qy 12 ThrleuMetlyLeuThrclyuAyrpArgInglInleArygIngllyLeuIngluInleuIn 31
Db 613 ACGGAATTCAAGAGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAG 672
Qy 32 LysValLeuProGlyGlyAyrPThrTyTwechIsGluGlyPheGluAyrAlaSerGluIn 51
Db 673 -----GGCCTGAGCTACACAGCCCTGGGATGACCAAGAGTGTGAAGAG 717
Qy 52 IleTyTyGluAenAyrGlnGlyTyTargThrAla---SerValIleIleAlaLeuThr 70
Db 718 CTAATTCATACAGCAAGATGGGCGCCGAAAGTGCAGAGAGATCTAATGTCATCACA 777
Qy 71 AyrGlyGluLeuHISgluAyrLeuPhePheTyTyrSerGlu-----ArgGluAlaAenAyr 88
Db 778 GATGGGCAAGAAATTCAGAGAGCCCTGGAGATATAGACATGTCATCCCTGAAAGAGAGAA 837
Qy 89 SerAyrAyrLeuGlyAlaIleValTyTyrCyValGlyValLyAyrP---PheAenGlu--- 106
Db 838 GCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTCCGGGAGACC 888
Qy 107 ThrGlnLeuAlaAyrGlie-----AlaAyrSerLyAyrPheHisValPhePro 121
Db 889 ACTGCCCTACAGAGAGCTGAAACCATGCTGCTCAGCTCCCTCCAGAGACAGCTGTTCAAG 948
Qy 122 ValAenAyrGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLyAyrSerCyS 141
Db 949 GTGGGCAT---TTTGTAGCACTTCGCAAGCATCCAGCGCAATTCAGAGAGAA----- 999
Qy 142 IleGluIleLeuAlaIleGluProSerThrIleCyValGlyGluSerPheGlnVal 161
Db 1000 -----ATCTTGTGCATTTGAAGAACCGAATCAAGTCAAGTATCTTTCCAGACAGAG 1053
Qy 162 ValAyrGlyAenGlyPheAyrGhiAlaAyrAenValAyr 174
Db 1054 ATGTCAAGAGAGTTTCAGCTCAGCTCTCTCAATGAT 1092

RESULT 14
US-08-605-672-52
; Sequence 52, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica

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TITLE OF INVENTION: No. 5817515e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES: 103
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 3803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3486
US-08-605-672-52
US-08-605-672-52
Alignment Scores:
Pred. No.: 6.72e-07 Length: 3803
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69
Query Match: 11.36% Indels: 23
Gaps: 9
US-09-970-076-10 (1-218) x US-08-605-672-52 (1-3803)
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QY 32 LysValleuProGlyGlyAspThrTyMetHlsglulYpHehluArgAlseerGluln 51
DB 673 -----GGCCTGACGTACACAGCCTCGGCGATCCAGAAAGTGTAAGAG 717
QY 52 lleyTYrGluAsnArgInclYTyArgThAla---SerVallelleAlaleuThr 70
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QY 89 SerArgAspleuGlYAlaIleValTYrCyseValGlyValIysAsp---PheAenglu--- 106
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QY 107 ThGlInleuAlaArgIle-----AlaAspSerIyAspHlslVAlPhePro 121
DB 889 ACTGCCCTACAGAGCGTGAACACCATTTGCTCAGCTCCCTCCGAGACACCGTTCACAG 948
QY 122 ValAsnAspGlyPheGlnAlaleuGInglylleIleHlserIleleuYslYsSerCyS 141
DB 949 GTGGGCAAT---TTTGTAGCATCTCCGAGCATCCAGCGCAATTTCAGAGAAA----- 999
QY 142 lIeGluIleleuAlaIagluProserThrIleCyAlaGlyIuSerPheGlnVal 161
DB 1000 -----ATCTTTCATGTGAAGACCAATCAAGGTCAAGTGTCTTCAGACAGAG 1053
QY 162 ValArgGlyAsnGlyPheArgHlslAlaAsnValAsp 174
DB 1054 ATGTCAAGAGAGTTTCAGCTCAGCTCTCTCATGTGAT 1092
RESULT 15
US-08-482-293A-52
Sequence 52, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vliet, Monica
TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 3803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3486
US-08-482-293A-52

Alignment Scores:

Pred. No.:	6,726-07	Length:	3803
Score:	128.50	Matches:	50
Percent Similarity:	46.82%	Conservative:	31
Best Local Similarity:	28.90%	Mismatches:	69
Query Match:	11.36%	Indels:	23
DB:	2	Gaps:	9

US-09-970-076-10 (1-218) x US-08-482-293A-52 (1-3803)

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DB      949 GTGGGCAAT---TTGTAGCACTTCGAGAGATCCAGCGGCAATTCAGAGAGAA----- 999
QY      142 IleGlnIleLeuAlaAlaGlnProSerThrIleCysAlaGlyGluSerPheGlnVal 161
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QY      162 ValArgGlyAsnGlyPheArgHisAlaArgAspValAsp 174
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 Job time : 57.4808 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 22, 2004, 02:37:46 ; Search time 324.721 Seconds

(without alignments)
3075.489 Million cell updates/sec

Title: US-09-970-076-10

Perfect score: 1131
Sequence: 1 MSFVFSRGTGTTMKLTEDR.....STSGKEGNSHPCLPAPHT 218

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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2	1131	100.0	1609	16	US-10-117-722-8	Sequence 8, Appl1
3	977	86.4	1534	15	US-10-201-292-33	Sequence 33, Appl1
4	966.5	85.5	1608	15	US-10-201-292-35	Sequence 33, Appl1
5	966	85.4	1008	15	US-10-038-307-25	Sequence 25, Appl1
6	966	85.4	1008	15	US-10-201-292-25	Sequence 25, Appl1
7	966	85.4	1047	15	US-10-038-307-21	Sequence 21, Appl1
8	966	85.4	1047	15	US-10-201-292-21	Sequence 21, Appl1
9	966	85.4	1056	15	US-10-038-307-23	Sequence 23, Appl1
10	966	85.4	1056	15	US-10-201-292-23	Sequence 23, Appl1
11	966	85.4	1454	16	US-10-133-337-58	Sequence 58, Appl1
12	966	85.4	1454	16	US-10-159-563-58	Sequence 58, Appl1
13	966	85.4	1623	15	US-10-038-307-11	Sequence 11, Appl1
14	966	85.4	1623	15	US-10-201-292-11	Sequence 11, Appl1
15	966	85.4	1650	15	US-10-038-307-9	Sequence 9, Appl1
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23	966	85.4	1713	15	US-10-038-307-19	Sequence 19, Appl1
24	966	85.4	1713	15	US-10-201-292-19	Sequence 19, Appl1
25	966	85.4	2272	10	US-09-796-753-11	Sequence 11, Appl1
26	966	85.4	2272	15	US-10-028-307-1	Sequence 1, Appl1
27	966	85.4	2272	15	US-10-201-292-1	Sequence 1, Appl1
28	966	85.4	2353	15	US-10-198-846-9957	Sequence 9957, Ap
29	966	85.4	2459	9	US-09-833-381-998	Sequence 998, App
30	966	85.4	5540	13	US-09-918-715-176	Sequence 176, App
31	966	85.4	5540	13	US-09-918-715-231	Sequence 231, App
32	966	85.4	5540	15	US-10-301-822-198	Sequence 198, App
33	960	84.9	5220	13	US-09-918-715-186	Sequence 186, App
34	960	84.9	5220	13	US-09-918-715-300	Sequence 300, App
35	938	82.9	2397	16	US-10-062-674-1757	Sequence 1757, Ap
36	878	77.6	1464	15	US-10-201-292-31	Sequence 31, Appl1
37	767	67.8	1401	15	US-10-201-292-27	Sequence 27, Appl1
38	767	67.8	1401	15	US-10-201-292-29	Sequence 29, Appl1
39	704	62.2	1650	14	US-10-047-542-98	Sequence 98, Appl1
40	704	62.2	6602	14	US-10-047-542-107	Sequence 107, App
41	571	50.5	454	16	US-10-062-674-117	Sequence 417, App
42	534	47.2	569	10	US-09-918-995-22508	Sequence 22508, A
43	506	44.7	977	16	US-10-264-237-169	Sequence 169, App
44	506	44.7	1492	16	US-10-120-988-297	Sequence 297, App
45	506	44.7	2026	16	US-10-094-749-495	Sequence 495, App

ALIGNMENTS

RESULT 1
US-10-037-270-8
; Sequence 8, Application US/10037270
; Publication No. US20030104529A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehtman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1 Nucleic Acids and

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; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 8
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (309)..(1202)
; US-10-037-270-8

Alignment Scores:
Pred. No.: 2,11e-145 Length: 1609
Score: 1131.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

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DB 546 ATGTCCTTATTGTTTCTCCACCCGAGAAACACTTAATGAACTGACAGAAAGACAGA 605
QY 21 GluGlnIleArgGlnGlyLeuGlnGluGlnIleValLeuProGlyValAspThrTyr 40
DB 606 GAACAAATCCGTCAGAGCCCTAGAAAGACTCCAGAAAGTTCTGCCAGAGGAGACACTTAC 665
QY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnLYTyr 60
DB 666 ATGCATGAAGGATTGAAAGGCCGAGTGAAGAGATTATTATGAAAACAGCAAGGGTAC 725
QY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
DB 726 AGGACAGCCAGCGTCATCATTTGCTTGACTGTGAGAACTCCATGAAGATCTCTTTTTC 785
QY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100
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DB 906 CCCGTAATGACGCGCTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCC 965
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; Sequence 8, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2B2CIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 8
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (309)..(1202)
; US-10-117-722-8

Alignment Scores:
Pred. No.: 2,11e-145 Length: 1609
Score: 1131.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

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QY 1 MetSerPheIleValPheSerThrArgLYThrThreumElyLeuThrGluAspArg 20
DB 546 ATGTCCTTATTGTTTCTCCACCCGAGAAACACTTAATGAACTGACAGAAAGACAGA 605
QY 21 GluGlnIleArgGlnGlyLeuGlnGluGlnIleValLeuProGlyValAspThrTyr 40
DB 606 GAACAAATCCGTCAGAGCCCTAGAAAGACTCCAGAAAGTTCTGCCAGAGGAGACACTTAC 665
QY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnLYTyr 60
DB 666 ATGCATGAAGGATTGAAAGGCCGAGTGAAGAGATTATTATGAAAACAGCAAGGGTAC 725
QY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
DB 726 AGGACAGCCAGCGTCATCATTTGCTTGACTGTGAGAACTCCATGAAGATCTCTTTTTC 785
QY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100
DB 786 TATTCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGCGCAATTGTTACTGTGTGGT 845
QY 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLYAspHisValPhe 120
DB 846 GTGAAAGATTTCAATGAGACACAGCTGGCCGGATGGCGACAGTAAGATCATGTGTTT 905
QY 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLYLysSer 140
DB 906 CCCGTAATGACGCGCTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCC 965
QY 141 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
DB 966 TGCATCGAAATTTCTAGCAGCTGAAACCATCCATATGTGCGAGAGAGTCAATTCAGAGT 1025
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Qy 161 ValValaRgGlyAenGlyPheArghIaIaRgaenValaAparGValleuCyseSerPhe 180
Db 1026 GTCTGAGAGAGAAAGCGCTTCCGACATCCCGACAGCGTGGACAGGCTCTTCGACGCTTC 1085
Qy 181 LysIleAenAapSerValThreusSerlySerleuGlnSerProTprValSerSerThr 200
Db 1086 AAGATCATGACTCGGTCACTCACTAGTAAAGTCTTGAGAGATCCATGGGTTCTTCGACA 1145
Qy 201 SerGlyPheYsgGlyAenSerHisProCyseuProAlaArgProHisThr 218
Db 1146 AGTGCTTCAAGAGAGAAATCCACCCCTTCTTCGACAGAGCCACACACA 1199

RESULT 3
US-10-201-292-33
; Sequence 33, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 1534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-33

Alignment Scores:
Pred. No.: 3,686-124 Length: 1534
Score: 977.00 Matches: 197
Percent Similarity: 92.65% Conservative: 5
Best Local Similarity: 90.37% Mismatches: 8
Query Match: 86.38% Indels: 8
Gaps: 3

US-09-970-076-10 (1-218) x US-10-201-292-33 (1-1534)
Qy 1 MetSerPheIleValPheSerThrArgGlyThrThreuMetlySeuThrgluAparG 20
Db 250 ATGTCCTTATTTGTTTCTCCACCCGAGAGAACCTTAATGAATGACAGAAAGACAGA 309
Qy 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnValleuProGlyGlyAspThrTyr 40
Db 310 GAACAAATCCGTCAAGGCTTAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTAC 369
Qy 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAenArgGlnGlyTyr 60
Db 370 ATGCATGAAGATTTGAAAGGCGCAGTGACGATTTATTAAGAAACAGACAGAGGATAC 429
Qy 61 ArgThrAlaSerValIleIleAlaLeuThraPrgGlyLeuHisGluAsePhePhe 80
Db 430 AGGACAGCCAGCGTCATCTTGTCTTGAATGAGAACTCCATGAAGATCTCTTTTTC 489
Qy 81 TyrSerGluArgGluAlaAenArgSerArgAspLeuGlyAlaIleValTyrCyseValGly 100
Db 490 TATTCAGAGAGGAGGCTTAATAGGCTTCGAAATCTTGAGCAATGTTTACTGTGTGGT 549
Qy 101 ValIlyAapPheAenGluThrgInleuAlaArgIleAlaAsePserlyAapHisValPhe 120
Db 550 GTGAAGATTTCAATGAGACACAGCGTGGCCGATGGCGACAGTAAAGATCATGTGTTT 609
Qy 121 ProValAenAapGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYalysSer 140
Db 610 CCCGGAATGACGCGCTTTCAGGCTCTGCAAGGACATCATCTCAATTTTGAAGAAGTCC 669
Qy 141 CysIleGluIleLeuAlaIleGluProSerThrIleCyseAlaGlyGluSerPheGlnVal 160

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Db 670 TGATCGAAATTTAGACAGCTGAACCATCCATATGTGACGAGAGATCTTCAAGTT 729
Qy 161 ValValaRgGlyAenGlyPheArghIaIaRgaenValaAparGValleuCyseSerPhe 180
Db 730 GTCTGAGAGAGAAAGCGCTTCCGACATCCCGACAGCGTGGACAGGCTCTTCGACGCTTC 789
Qy 181 LysIleAenAapSerValThreusSerlySerleuGlnSerProTprValSerSerThr 200
Db 790 AAGTCAATGACTCGGTCACTCACTAATGAGAAAGCCCTTCTCCCAAATC----- 840
Qy 201 SerGlyPheYsgGlyAenSerHisProCyseuProAlaArgProHisThr 218
Db 841 -----TTTCGACAA-----AACTCACAC-----ATGCCACCGTGGCCAGCACC 879

RESULT 4
US-10-201-292-35
; Sequence 35, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 1608
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-35

Alignment Scores:
Pred. No.: 1,126-122 Length: 1608
Score: 966.50 Matches: 194
Percent Similarity: 93.18% Conservative: 11
Best Local Similarity: 88.18% Mismatches: 11
Query Match: 85.46% Indels: 5
Gaps: 2

US-09-970-076-10 (1-218) x US-10-201-292-35 (1-1608)
Qy 1 MetSerPheIleValPheSerThrArgGlyThrThreuMetlySeuThrgluAparG 20
Db 250 ATGTCCTTATTTGTTTCTCCACCCGAGAGAACCTTAATGAATGACAGAAAGACAGA 309
Qy 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnValleuProGlyGlyAspThrTyr 40
Db 310 GAACAAATCCGTCAAGGCTTAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTAC 369
Qy 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAenArgGlnGlyTyr 60
Db 370 ATGCATGAAGATTTGAAAGGCGCAGTGACGATTTATTAAGAAACAGACAGAGGATAC 429
Qy 61 ArgThrAlaSerValIleIleAlaLeuThraPrgGlyLeuHisGluAsePhePhe 80
Db 430 AGGACAGCCAGCGTCATCTTGTCTTGAATGAGAACTCCATGAAGATCTCTTTTTC 489
Qy 81 TyrSerGluArgGluAlaAenArgSerArgAspLeuGlyAlaIleValTyrCyseValGly 100
Db 490 TATTCAGAGAGGAGGCTTAATAGGCTTCGAAATCTTGAGCAATGTTTACTGTGTGGT 549
Qy 101 ValIlyAapPheAenGluThrgInleuAlaArgIleAlaAsePserlyAapHisValPhe 120
Db 550 GTGAAGATTTCAATGAGACACAGCGTGGCCGATGGCGACAGTAAAGATCATGTGTTT 609
Qy 121 ProValAenAapGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYalysSer 140
Db 610 CCCGGAATGACGCGCTTTCAGGCTCTGCAAGGACATCATCTCAATTTTGAAGAAGTCC 669

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Oy 141 CysileglluleuAlaIaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
Db 670 TGCATCGAAATTTCTAGCAGCTTACCACTCCACCATATGTGACAGAGATCTTTCAAGTT 729
Oy 161 ValValaIaArgGlyAanglyPheArgHisAlaIaArgAsnValaIaPArgValleuCysSerPhe 180
Db 730 GTCCGAGAGAGAAACGGCTTCCGACATGCCCGCAACGTGACAGGGCTCTCTGCAGCTTC 789
Oy 181 LysIleAsnAspSerValThrIleuSerLys-----SerLeuGlnSerProThrVal 197
Db 790 AAGATCAATGACTCGCTCACTCACTCAATGAAAGCCCTTTCTGTGGAAAGATCTTATT- 848
Oy 198 SerSerThrSerGlyPheLysGluGlyAsnSerHis---ProCysLeuProAlaArgPro 216
Db 849 ACTGTGTCACGCGCTATCTTAAAGAAGTTGGCATGAAGCTGCACCTCAGGTCAGCC 908

RESULT 5
US-10-038-307-25
; Sequence 25, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-25

Alignment Scores:
Pred. No.: 6,356-123 Length: 1008
Score: 966.00 Matches: 188
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match: 85.41% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-038-307-25 (1-1008)
Oy 1 MetSerPheIleValIlePheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArg 20
Db 250 ATGTCCTTATTTGTTTCTCCACCCGAGGAACAACCTTAATGAACCTGACAGAAAGACAGA 309
Oy 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnLysValIleuProGlyGlyAspThrTyr 40
Db 310 GAACAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGGAGAGACACTTAC 369
Oy 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
Db 370 ATGCATGAAGATTGGAAGAGCCGACGTGACGATTTTATGAAAACAGACAGAGGTAC 429
Oy 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
Db 430 AGGACAGCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAGATCTCTTTTC 489
Oy 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyValaIleValTyrCysValGly 100
Db 490 TATTGAGAGAGGAGGCTTAATAGCTCTGAGATCTTGACATTTGTTACTGTGTGGT 549
Oy 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120
Db 550 GTGAAAGATTTTCATGAGACACAGCTGCCGCGATTCGGACAGTAAAGATCATGTGTTT 609
Oy 121 ProValaAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 140
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Db 610 CCCGTGAATACGGCTTTCAGGCTTCGCAAGGATCATCTCACTCAATTTGAAAGAACTCC 669
Oy 141 CysileglluleuAlaIaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
Db 670 TGCATCGAAATTTCTAGCAGCTTACCACTCCACCATATGTGACAGAGATCTTTCAAGTT 729
Oy 161 ValValaIaArgGlyAanglyPheArgHisAlaIaArgAsnValaIaPArgValleuCysSerPhe 180
Db 730 GTCCGAGAGAGAAACGGCTTCCGACATGCCCGCAACGTGACAGGGCTCTCTGCAGCTTC 789
Oy 181 LysIleAsnAspSerValThrIleuSerLys 190
Db 790 AAGATCAATGACTCGCTCACTCACTCAATGAG 819

RESULT 6
US-10-201-292-25
; Sequence 25, Application US/10201292
; Publication No. US2003014193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-25

Alignment Scores:
Pred. No.: 6,356-123 Length: 1008
Score: 966.00 Matches: 188
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match: 85.41% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-201-292-25 (1-1008)
Oy 1 MetSerPheIleValIlePheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArg 20
Db 250 ATGTCCTTATTTGTTTCTCCACCCGAGGAACAACCTTAATGAACCTGACAGAAAGACAGA 309
Oy 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnLysValIleuProGlyGlyAspThrTyr 40
Db 310 GAACAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGGAGAGACACTTAC 369
Oy 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
Db 370 ATGCATGAAGATTGGAAGAGCCGACGTGACGATTTATATGAAAACAGACAGAGGTAC 429
Oy 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
Db 430 AGGACAGCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAGATCTCTTTTC 489
Oy 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyValaIleValTyrCysValGly 100
Db 490 TATTGAGAGAGGAGGCTTAATAGCTCTGAGATCTTGTCATTTGTTACTGTGTGGT 549
Oy 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120
Db 550 GTGAAAGATTTTCATGAGACACAGCTGCCGCGATTCGGACAGTAAAGATCATGTGTTT 609
Oy 121 ProValaAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 140
Db 610 CCCGTGAATACGGCTTTCAGGCTTCGCAAGGATCATCTCACTCAATTTGAAAGAACTCC 669
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141 CysllleagluleuAlaIleuProserThrIleCyAlaGlyGlySerPheGlnVal 160
Db 670 TGCATCGAAATTTCTAGCAGCTGACCACTCCATATGTCAGGAGCTTTCAAGTT 729
Qy 161 ValValaArgGlyAenGlyPheArgHlaIaArgaenValaAspaArgValIleuCySerPhe 180
Db 730 GTCGTGAGAGGAAACGGCTTCGACATGCGCCGCAACGTGACAGGGTCTCTGACAGCTTC 789
Qy 181 LysIleAenAserValThrIleuSerLys 190
Db 790 AAGATCAATGACTCGCTCACACTCAATGAG 819

RESULT 7
US-10-038-307-21
; Sequence 21, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-21

Alignment Scores:
Pred. No.: 6,73e-123 Length: 1047
Score: 966.00 Matches: 188
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match: 85.41% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-038-307-21 (1-1047)

Qy 1 MetSerPheIleValIlePheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspaArg 20
Db 277 ATGTCCTTATTTGTTTCTCCACCCGAGAACACCTTAATGAACTGACAGAAACAGCA 336
Qy 21 GluGlnIleArgGlnGlyLeuGlnIleuGlnIleuValIleuProGlyGlyAspThrTyr 40
Db 337 GAACAAATCCGTCAGAGGCTTAGAGAACTCCAGAAAGTTCTCCAGAGAGAGACACTTAC 396
Qy 41 MethIleGlnGlyPheGlnIleuArgIleuArgIleuTyrTyrGluAsnaArgGlnGlyTyr 60
Db 397 ATGCATGAAGATTTGAAAGGCGCCAGTGACAGATTTATTAAGAAACAGACAGAGGTAC 456
Qy 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHicGluAspLeuPhePhe 80
Db 457 AGGACAGCCAGCGTCATCATTCCTTGACTGATGGAACCTCATGAAGATCTCTTTTTC 516
Qy 81 TyrSerGluArgGluAlaAsnaArgSerArgAspLeuGlyAlaIleValTyrCyAlaGly 100
Db 517 TATTCAGAGAGGAGGCTTAATAGGTCGAGATCTTGAGCAATGTTTACTGTGTGGT 576
Qy 101 ValIlyAspPheAsnGlnThrGlnIleuAlaArgIleAlaAspSerLysAspHlaValPhe 120
Db 577 GTGAAAGATTTCAATGACACACAGCTGCGCGGATTCGCGACAGTAAGATCATGTGTTT 636
Qy 121 ProValaAsnaArgGlyPheGlnAlaIleuGlnGlyIleIleHicSerIleLeuLysLysSer 140
Db 637 CCCGGAATGACGGCTTCAAGCTCTGCAAGGACATCTCACTCAATTTTGAAGAGTCC 696
Qy 141 CysIleGlnIleuAlaIleGluProserThrIleCyAlaGlyGlySerPheGlnVal 160

161 ValValaArgGlyAenGlyPheArgHlaIaArgaenValaAspaArgValIleuCySerPhe 180
Db 757 GTCGTGAGAGGAAACGGCTTCGACATGCGCCGCAACGTGACAGGGTCTCTGACAGCTTC 816
Qy 181 LysIleAenAserValThrIleuSerLys 190
Db 817 AAGATCAATGACTCGCTCACACTCAATGAG 846

RESULT 8
US-10-201-292-21
; Sequence 21, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-21

Alignment Scores:
Pred. No.: 6,73e-123 Length: 1047
Score: 966.00 Matches: 188
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match: 85.41% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-201-292-21 (1-1047)

Qy 1 MetSerPheIleValIlePheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspaArg 20
Db 277 ATGTCCTTATTTGTTTCTCCACCCGAGAACACCTTAATGAACTGACAGAAACAGCA 336
Qy 21 GluGlnIleArgGlnGlyLeuGlnIleuGlnIleuValIleuProGlyGlyAspThrTyr 40
Db 337 GAACAAATCCGTCAGAGGCTTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTAC 396
Qy 41 MethIleGlnGlyPheGlnIleuArgIleuArgIleuTyrTyrGluAsnaArgGlnGlyTyr 60
Db 397 ATGCATGAAGATTTGAAAGGCGCCAGTGACAGATTTATTAAGAAACAGACAGAGGTAC 456
Qy 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHicGluAspLeuPhePhe 80
Db 457 AGGACAGCCAGCGTCATCATTCCTTGACTGATGGAACCTCATGAAGATCTCTTTTTC 516
Qy 81 TyrSerGluArgGluAlaAsnaArgSerArgAspLeuGlyAlaIleValTyrCyAlaGly 100
Db 517 TATTCAGAGAGGAGGCTTAATAGGTCGAGATCTTGAGCAATGTTTACTGTGTGGT 576
Qy 101 ValIlyAspPheAsnGlnThrGlnIleuAlaArgIleAlaAspSerLysAspHlaValPhe 120
Db 577 GTGAAAGATTTCAATGACACACAGCTGCGCGGATTCGCGACAGTAAGATCATGTGTTT 636
Qy 121 ProValaAsnaArgGlyPheGlnAlaIleuGlnGlyIleIleHicSerIleLeuLysLysSer 140
Db 637 CCCGGAATGACGGCTTCAAGCTCTGCAAGGACATCTCACTCAATTTTGAAGAGTCC 696
Qy 141 CysIleGlnIleuAlaIleGluProserThrIleCyAlaGlyGlySerPheGlnVal 160
Db 697 TGCATCGAAATTTCTAGCAGCTGACCACTCCATATGTCAGGAGAGTCTTCAAGTT 756

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Oy 161 ValValaArgGlyAsnGlyPheArgHisAlaArgAsnValaAspArgValleuCysSerPhe 180
Db 757 GTCGTGAAGAGAAACGGCTTCGACATGCCCGAACAAGTGCAGAGGCTCTCTGCACGCTTC 816
Oy 181 LysIleAsnAspSerValThrIleuSerLys 190
Db 817 AAGATCAATGACTCGGTCACTCACTCAATGAG 846

RESULT 9
US-10-038-307-23
; Sequence 23, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANNAK
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-23

Alignment Scores:
Pred. No.: 6,82e-123 Length: 1056
Score: 966.00 Matches: 188
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match: 85.41% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-038-307-23 (1-1056)
Oy 1 MetSerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArg 20
Db 250 ATGTCCTTTATTTGTTTCTCCACCGAGAAACMACTTAATGAACCTGACGAAGACGA 309
Oy 21 GluGlnIleArgGlnGlyLeuGlnGluLeuGlnLysValleuProGlyGlyAspThrTyr 40
Db 310 GAACAAATCCGTCAAGGCTTAGAAGAACTCCGAAGATTTCTGCCAGGAGAGACACTTAC 369
Oy 41 MetHisGlnGlyPheGluArgAlaSerGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
Db 370 ATGCATGAAGATTGGAAGAGGCCGAGTGAGCATTTATTAAGAAAACAGCAAGGGTAC 429
Oy 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
Db 430 AGGACAGCCAGGCTCATCTGCTTGAAGTGAAGAACCTCCAGAAAGATCTCTTTTC 489
Oy 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100
Db 490 TATTACAGAGAGGAGCTTAATAGTCTGAGATCTTGTCATTTGTTTACTGCTGTTGCT 549
Oy 101 ValIlyAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120
Db 550 GTGAAGAATTTCAATGAGACACAGCTGGCCGGATTCGGACAGTAAGATCATGCTGTTT 609
Oy 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140
Db 610 CCCGTGAATGACGGCTTTCAGGCTTCGACAGGCATCATCTCAATTTTGAAGAGTCC 669
Oy 141 CysIleGlnIleLeuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGlnVal 160
Db 670 TGCAATCAAAATTTCTAGACGCTGACCAATCCACCATATGTGAGGAGGTCTTTCAATTT 729
Oy 161 ValValaArgGlyAsnGlyPheArgHisAlaArgAsnValaAspArgValleuCysSerPhe 180
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Db 730 GTCGTGAAGAGAAACGGCTTCGACATGCCCGAACAAGTGCAGAGGCTCTCTGCACGCTTC 789
Oy 181 LysIleAsnAspSerValThrIleuSerLys 190
Db 790 AAGATCAATGACTCGGTCACTCACTCAATGAG 819

RESULT 10
US-10-201-292-23
; Sequence 23, Application US/10201292
; Publication No. US2003014193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-23

Alignment Scores:
Pred. No.: 6,82e-123 Length: 1056
Score: 966.00 Matches: 188
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match: 85.41% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-201-292-23 (1-1056)
Oy 1 MetSerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArg 20
Db 250 ATGTCCTTTATTTGTTTCTCCACCGAGAAACMACTTAATGAACCTGACGAAGACGA 309
Oy 21 GluGlnIleArgGlnGlyLeuGlnGluLeuGlnLysValleuProGlyGlyAspThrTyr 40
Db 310 GAACAAATCCGTCAAGGCTTAGAAGAACTCCGAAGATTTCTGCCAGGAGAGACACTTAC 369
Oy 41 MetHisGlnGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
Db 370 ATGCATGAAGATTGGAAGAGGCCGAGTGAGCATTTATTAAGAAAACAGCAAGGGTAC 429
Oy 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
Db 430 AGGACAGCCAGGCTCATCTGCTTGAAGTGAAGAACCTCCAGAAAGATCTCTTTTC 489
Oy 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100
Db 490 TATTACAGAGAGGAGCTTAATAGTCTGAGATCTTGTCATTTGTTTACTGCTGTTGCT 549
Oy 101 ValIlyAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120
Db 550 GTGAAGAATTTCAATGAGACACAGCTGGCCGGATTCGGACAGTAAGATCATGCTGTTT 609
Oy 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140
Db 610 CCCGTGAATGACGGCTTTCAGGCTTCGACAGGCATCATCTCAATTTTGAAGAGTCC 669
Oy 141 CysIleGlnIleLeuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGlnVal 160
Db 670 TGCAATCAAAATTTCTAGACGCTGACCAATCCACCATATGTGAGGAGGTCTTTCAATTT 729
Oy 161 ValValaArgGlyAsnGlyPheArgHisAlaArgAsnValaAspArgValleuCysSerPhe 180
Db 730 GTCGTGAAGAGAAACGGCTTCGACATGCCCGAACAAGTGCAGAGGCTCTCTGCACGCTTC 789
```


QY 181 LysilleaanaaPseValThrluSerlys 190
DB 790 AAGATCAATGACTCGCTCACCTCAATGAG 819

RESULT 11
US-10-133-937-58
Sequence 58, Application US/10133937
Publication No. US20030207278A1
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING, DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
FILE REFERENCE: 11613.56US01
CURRENT APPLICATION NUMBER: US/10/133,937
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 1454
TYPE: DNA
ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:
Pred. No.: 1.12e-122 Length: 1454
Score: 966.00 Matches: 188
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match: 85.41% Indels: 0
DB: 16 Gaps: 0

US-09-970-076-10 (1-218) x US-10-133-937-58 (1-1454)

QY 1 MetSerPheIleValPheSerThrArgGlyThrThrluMetClyleuThrGluAspArg 20
DB 381 ATGTCCTTATTTGTTTCTCCACCGAGAGACAACTTAATGAACAGACAGAAACAGA 440

QY 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnValLeuProGlyGlyAspThrTyr 40
DB 441 GAACAAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTCCAGAGAGACACTTAC 500

QY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
DB 501 ATGCATGAAGATTTGAAAGGCGCACTGAGCATTTATTATGAAGAAACAGACAGAGGTAC 560

QY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
DB 561 AGGACAGCCAGCGTCATCTGCTTGAAGTGAAGAGAACTCATGAGAGATCTCTTTTTC 620

QY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100
DB 621 TATTCAGAGAGGAGGCTTAATAGGTCGAGATCTTGAGCAATGTTTACTGCTGTGCT 680

QY 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120
DB 681 GTGAAGATTTCAATGAGACACAGCTGCCCGGATTTGGCGGACAGTAAGATCATGTGTTT 740

QY 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140
DB 741 CCCGTAATGACGGCTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAGATCC 800

QY 141 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
DB 801 TGCATGAAATTTCTAGCAGCTGAACCATCACCATATGTGACAGAGATCATTTCAAGTT 860

QY 161 ValIleArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPhe 180
DB 861 GTCGTGAGAGAGAGGCTTCCGACATGCTCCGCAAGTGTGAGACAGGCTCTCTGCAAGCTTC 920

QY 181 LysilleaanaaPseValThrluSerlys 190
DB 921 AAGATCAATGACTCGCTCACCTCAATGAG 950

RESULT 12
US-10-159-563-58
Sequence 58, Application US/10159563
Publication No. US20040009154A1
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
FILE REFERENCE: 11613.56US11
CURRENT APPLICATION NUMBER: US/10/159,563
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 444
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 1454
TYPE: DNA
ORGANISM: Homo sapiens
US-10-159-563-58

Alignment Scores:
Pred. No.: 1.12e-122 Length: 1454
Score: 966.00 Matches: 188
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match: 85.41% Indels: 0
DB: 16 Gaps: 0

US-09-970-076-10 (1-218) x US-10-159-563-58 (1-1454)

QY 1 MetSerPheIleValPheSerThrArgGlyThrThrluMetClyleuThrGluAspArg 20
DB 381 ATGTCCTTATTTGTTTCTCCACCGAGAGACAACTTAATGAACAGACAGAAACAGA 440

QY 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnValLeuProGlyGlyAspThrTyr 40
DB 441 GAACAAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTCCAGAGAGACACTTAC 500

QY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
DB 501 ATGCATGAAGATTTGAAAGGCGCACTGAGCATTTATTATGAAGAAACAGACAGAGGTAC 560

QY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
DB 561 AGGACAGCCAGCGTCATCTGCTTGAAGTGAAGAGAACTCATGAGAGATCTCTTTTTC 620

QY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100
DB 621 TATTCAGAGAGGAGGCTTAATAGGTCGAGATCTTGAGCAATGTTTACTGCTGTGCT 680

QY 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120
DB 681 GTGAAGATTTCAATGAGACACAGCTGCCCGGATTTGGCGGACAGTAAGATCATGTGTTT 740

QY 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140
DB 741 CCCGTAATGACGGCTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAGATCC 800

QY 141 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
DB 801 TGCATGAAATTTCTAGCAGCTGAACCATCACCATATGTGACAGAGATCATTTCAAGTT 860

QY 161 ValIleArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPhe 180

Db 861 GTCGTGAGAGAAACGGCTTCGACATGCCGCAACGTGACAGGGCTCTCTGCAGCTTC 920
Qy 181 LysileuAaspSerValThrleuSerLys 190
Db 921 AAGATCAATGACTCGGTCACTCACTCAATGAG 950

RESULT 13

US-10-038-307-11
; Sequence 11, Application US/10038307
; Publication No. US20030134786A1
GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-11

Alignment Scores:

Pred. No.:	1,33e-122	Length:	1623
Score:	966.00	Matches:	188
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	98.95%	Mismatches:	0
Query Match:	85.41%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-10 (1-218) x US-10-038-307-11 (1-1623)

Qy 1 MetSerPheIleValPheSerThrArgLgLYThrThreumetLysleuThrgluAaspArg 20
Db 211 ATGTCCTTATTGTTTCTCCACCCGAGAACAACTTAATGAACTGACAGAAAGACAGA 270
Qy 21 GUGUlnleArgGlnGlyLeuGluGluLeuGlnLysValleuProGlyGlyAaspThrTyr 40
Db 271 GAACAAATCCGTCAGAGGCTAGAAAGACTCCAGAAAGTTCTCCGAGGAGACACTTAC 330
Qy 41 MethisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAaspArgGlnGlyTyr 60
Db 331 ATGCATGAAGATTGAAAGGCCGAGTGAAGATTTATTGAAAACAGACAAAGGTAC 390
Qy 61 ArgThrAlaSerValIleIleAlaLeuThrAaspGlyGluLeuHisGluAaspLeuPhePhe 80
Db 391 AGGACAGCCAGCGTCATCTGCTTGAAGTGAAGAACATCCAGAAAGATCTCTTTTTC 450
Qy 81 TyrSerGluArgGluAlaAaspArgSerArgAaspLeuGlyAlaIleValTyrCyValGly 100
Db 451 TATTCAAGAGAGGAGCTTAATAGTCTGAGATCTTGCTATGCTTACTGTGTGCT 510
Qy 101 ValLysAaspPheAaspGluThrGlnLeuAlaArgIleAlaAaspSerLysAaspHisValPhe 120
Db 511 GTGAAAGATTTCAATGAGACACAGCTGGCCGAGTTGCGAGACAGTAAGATCATGTGTTT 570
Qy 121 ProValAaspArgLysPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140
Db 571 CCCCGAATAGACGGCTTTCAGGCTCTGCAAGCATCACTCAATTTTGAAGAAGTCC 630
Qy 141 CysIleGluIleLeuAlaAlaGluProSerThrIleCyValaGlyGluSerPheGlnVal 160
Db 631 TGCAATCAAAATTTCTAGCAAGCTGAACCATCCCAATATGTGACAGAGACTCATTTCAAGTT 690
Qy 161 ValValaArgGlyAaspGlyPheArgHisAlaArgAaspValAaspArgValLeuCySerPhe 180
Db 691 GTGCTGAGAGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGCAAGCTTC 750

Qy 181 LysileuAaspSerValThrleuSerLys 190
Db 751 AAGATCAATGACTCGGTCACTCACTCAATGAG 780

RESULT 14

US-10-201-292-11
; Sequence 11, Application US/10201292
; Publication No. US20030144193A1
GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-11

Alignment Scores:

Pred. No.:	1,33e-122	Length:	1623
Score:	966.00	Matches:	188
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	98.95%	Mismatches:	0
Query Match:	85.41%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-10 (1-218) x US-10-201-292-11 (1-1623)

Qy 1 MetSerPheIleValPheSerThrArgLgLYThrThreumetLysleuThrgluAaspArg 20
Db 211 ATGTCCTTATTGTTTCTCCACCCGAGAACAACTTAATGAACTGACAGAAAGACAGA 270
Qy 21 GUGUlnleArgGlnGlyLeuGluGluLeuGlnLysValleuProGlyGlyAaspThrTyr 40
Db 271 GAACAAATCCGTCAGAGGCTAGAAAGACTCCAGAAAGTTCTCCGAGGAGACACTTAC 330
Qy 41 MethisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAaspArgGlnGlyTyr 60
Db 331 ATGCATGAAGATTGAAAGGCCGAGTGAAGATTTATTGAAAACAGACAAAGGTAC 390
Qy 61 ArgThrAlaSerValIleIleAlaLeuThrAaspGlyGluLeuHisGluAaspLeuPhePhe 80
Db 391 AGGACAGCCAGCGTCATCTGCTTGAAGTGAAGAACATCCAGAAAGATCTCTTTTTC 450
Qy 81 TyrSerGluArgGluAlaAaspArgSerArgAaspLeuGlyAlaIleValTyrCyValGly 100
Db 451 TATTCAAGAGAGGAGCTTAATAGTCTGAGATCTTGCTATGCTTACTGTGTGCT 510
Qy 101 ValLysAaspPheAaspGluThrGlnLeuAlaArgIleAlaAaspSerLysAaspHisValPhe 120
Db 511 GTGAAAGATTTCAATGAGACACAGCTGGCCGAGTTGCGAGACAGTAAGATCATGTGTTT 570
Qy 121 ProValAaspArgLysPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140
Db 571 CCCCGAATAGACGGCTTTCAGGCTCTGCAAGCATCACTCAATTTTGAAGAAGTCC 630
Qy 141 CysIleGluIleLeuAlaAlaGluProSerThrIleCyValaGlyGluSerPheGlnVal 160
Db 631 TGCAATCAAAATTTCTAGCAAGCTGAACCATCCCAATATGTGACAGAGACTCATTTCAAGTT 690
Qy 161 ValValaArgGlyAaspGlyPheArgHisAlaArgAaspValAaspArgValLeuCySerPhe 180
Db 691 GTGCTGAGAGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGCAAGCTTC 750

Db 751 AAGATCAATGACTCGTCACACTCAATGAG 780

RESULT 15

US-10-038-307-9

/ Sequence 9, Application US/10038307
/ Publication No. US20030134786A1

GENERAL INFORMATION:

/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKANAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/038,307
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 1650
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-038-307-9

Alignment Scores:

Pred. No.:	1,366-122	Length:	1650
Score:	966.00	Matches:	188
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	98.95%	Mismatches:	0
Query Match:	85.41%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-10 (1-218) x US-10-038-307-9 (1-1650)

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QY 1 MetSerPheIleValPheSerThrArgGlyThrThrLeuMetIleValLeuThrGluAspArg 20
   |||||
Db 238 ATGTCCTTATGTTTCTCCACCCGAGGAAACACTTAATGAACTGACGAGAGACAGA 297

QY 21 GluGlnIleArgGlnGlyLeuGlnGluLeuGlnValLeuProGlyGlyAspThrTyr 40
   |||||
Db 298 GAACTAATCCGTCAGAGCCCTAGAAAGACTCCAGAAAGTTCTGCCAGAGAGACACTTAC 357

QY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
   |||||
Db 358 ATGCATGAAGATTGAAAGGCCCAAGTGAAGATTTATGAAACAGACAAAGGTAC 417

QY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
   |||||
Db 418 AGGACAGCCAGCGTCATCATGCTTTGACTGATGAGAACTCCATGAAGATCTTTTTC 477

QY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100
   |||||
Db 478 TATTGAGAGAGGAGGCTTAATAGTCTCGAGATCTTGCGCAATGTTACTGTGTGCT 537

QY 101 ValIleAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIleAspHisValPhe 120
   |||||
Db 538 GTGAAGAATTTCATGACAGACACAGCTGCCCCGATTCGCGACAGTAAGATCATGTCTT 597

QY 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleLysSer 140
   |||||
Db 598 CCCGTAATGACGGCTTCAGGCTCTGCAGGCAATCATCACTCAATTTTGAAGAGTCC 657

QY 141 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
   |||||
Db 658 TGCATCGAATTTCTAGCAGCTGACCAATCCATCATATGTCAGAGAGTCATTCAAGTT 717

QY 161 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPhe 180
   |||||
Db 718 GTCCGAGAGGAAAGGCTTCGACATGCGCGCAACGTGACAGGGTCTCTGACGCTTC 777

QY 181 LysIleAsnAspSerValThrLeuSerLys 190
   |||||
Db 778 AAGATCAATGACTCGTCACACTCAATGAG 807
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Search completed: June 22, 2004, 08:11:33
Job time : 329.721 secs

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Db 205 TEFKSLSPQSLVDIAIVQLQ-----GLTYTASGIQKVKELFHSNGARKSAKKILIVIT 259
QY 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGVND-FNE-TQLARI-----ADSKDHVP 121
Db 260 DGQKFRDPLEYRHVYIPEAEKA---GIRYALGVGDAPREFPALDELNTIGSAPQDHVFK 316
QY 122 VNDGFOLQGIHSLKSCIEILAAEPSTICAGESFOVVVRGNGFRRHARNVD 174
Db 317 VGN-FVALRSIORQIOERK-----IFAIEGTESRSSSSFOHEMSQBFSSALSM 364

RESULT 2
US-08-485-618-46
; Sequence 46, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485.618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-618-46

Query Match 11.4%; Score 128.5; DB 1; Length 1155;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

QY 12 TLMKLTEDREQIRGLBELQKVLPGDPTVMHEGFRASEQIYYENRGYRTA-SVIALT 70
Db 205 TEFKSLSPQSLVDIAIVQLQ-----GLTYTASGIQKVKELFHSNGARKSAKKILIVIT 259
QY 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGVND-FNE-TQLARI-----ADSKDHVP 121
Db 260 DGQKFRDPLEYRHVYIPEAEKA---GIRYALGVGDAPREFPALDELNTIGSAPQDHVFK 316

QY 122 VNDGFOLQGIHSLKSCIEILAAEPSTICAGESFOVVVRGNGFRRHARNVD 174
Db 317 VGN-FVALRSIORQIOERK-----IFAIEGTESRSSSSFOHEMSQBFSSALSM 364

RESULT 3
US-08-362-652-46
; Sequence 46, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362.652
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-362-652-46

Query Match 11.4%; Score 128.5; DB 1; Length 1155;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

QY 12 TLMKLTEDREQIRGLBELQKVLPGDPTVMHEGFRASEQIYYENRGYRTA-SVIALT 70
Db 205 TEFKSLSPQSLVDIAIVQLQ-----GLTYTASGIQKVKELFHSNGARKSAKKILIVIT 259
QY 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGVND-FNE-TQLARI-----ADSKDHVP 121
Db 260 DGQKFRDPLEYRHVYIPEAEKA---GIRYALGVGDAPREFPALDELNTIGSAPQDHVFK 316
QY 122 VNDGFOLQGIHSLKSCIEILAAEPSTICAGESFOVVVRGNGFRRHARNVD 174
Db 317 VGN-FVALRSIORQIOERK-----IFAIEGTESRSSSSFOHEMSQBFSSALSM 364

RESULT 4
US-08-605-672-46
; Sequence 46, Application US/08605672
; Patent No. 5817515

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-46

Query Match 11.4%; Score 128.5; DB 2; Length 1155;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

QY 12 TLMKLTEDREQIRGLEBLQKVLPGSDTYMEGFERASEQIYENRQGRTA-SVITALT 70
DB 205 TEFKSLSPQSLVDAIVQLQ-----GLTYTASGIQKVKELFHSKNGARKSAKKILIVIT 259
QY 71 DGEIHEDLFFYSE--REANRSRDLCATYVGVKD-FNE-TOLARI-----ADSKDHVP 121
DB 260 DQQRDPLEYRHVYPEAKA---GIRYALGVDAFEPYALQELNTIGSAPSDHVPK 316

QY 122 VNDGFQALQGIHSLIKKSCIEILAEPTICAGSFQVYVNGNFRHARNVD 174
DB 317 VGN-FVALRSIQROIQEK-----IFAIEGTESRSSSSFQHEMSQEGFSALSMD 364

RESULT 5
US-08-482-293A-46
Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-46

Query Match 11.4%; Score 128.5; DB 2; Length 1155;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

QY 12 TLMKLTEDREQIRGLEBLQKVLPGSDTYMEGFERASEQIYENRQGRTA-SVITALT 70
DB 205 TEFKSLSPQSLVDAIVQLQ-----GLTYTASGIQKVKELFHSKNGARKSAKKILIVIT 259
QY 71 DGEIHEDLFFYSE--REANRSRDLCATYVGVKD-FNE-TOLARI-----ADSKDHVP 121
DB 260 DQQRDPLEYRHVYPEAKA---GIRYALGVDAFEPYALQELNTIGSAPSDHVPK 316

QY 122 VNDGFQALQGIHSLIKKSCIEILAEPTICAGSFQVYVNGNFRHARNVD 174
DB 317 VGN-FVALRSIQROIQEK-----IFAIEGTESRSSSSFQHEMSQEGFSALSMD 364

RESULT 6
US-08-943-363-46
Sequence 46, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-943-363-46

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Query Match 11.4%; Score 128.5; DB 2; Length 1155;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TMKLTREDRQIQGLEELQKVLPGSDTYMHGEPERASEQIYYENRGQYRTA-SVITALT 70
Db 205 TEFKSSLSPPQSLVDATVQLQ-----GLTYTASGIQKVKELFHSKNGARKSACKILIVIT 259
Qy 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGVD--FNE--TOLARI-----ADSKDHVP 121
Db 260 DGQKFRDPLRYRVHVIPEAKA---GIIRYALGVDAFREPTALQELNTISAPSQDHVFK 316
Qy 122 VNDGFOALQGIHSLKSCIEILAAEPSTTCAGESFOVVVRNGGFRHARNVD 174
Db 317 VGN-FVALRSIORQIOEK----IFAIEGTESRSSSSFOHEMSQGFSSALSMD 364

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RESULT 7
US-09-193-043-46
; Sequence 46, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46

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; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-193-043-46
Query Match 11.4%; Score 128.5; DB 3; Length 1155;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TMKLTREDRQIQGLEELQKVLPGSDTYMHGEPERASEQIYYENRGQYRTA-SVITALT 70
Db 205 TEFKSSLSPPQSLVDATVQLQ-----GLTYTASGIQKVKELFHSKNGARKSACKILIVIT 259
Qy 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGVD--FNE--TOLARI-----ADSKDHVP 121
Db 260 DGQKFRDPLRYRVHVIPEAKA---GIIRYALGVDAFREPTALQELNTISAPSQDHVFK 316
Qy 122 VNDGFOALQGIHSLKSCIEILAAEPSTTCAGESFOVVVRNGGFRHARNVD 174
Db 317 VGN-FVALRSIORQIOEK----IFAIEGTESRSSSSFOHEMSQGFSSALSMD 364

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RESULT 8
US-09-688-307A-46
; Sequence 46, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-307A-46

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Query Match 11.4%; Score 128.5; DB 4; Length 1155;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TMKLTREDRQIQGLEELQKVLPGSDTYMHGEPERASEQIYYENRGQYRTA-SVITALT 70
Db 205 TEFKSSLSPPQSLVDATVQLQ-----GLTYTASGIQKVKELFHSKNGARKSACKILIVIT 259
Qy 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGVD--FNE--TOLARI-----ADSKDHVP 121
Db 260 DGQKFRDPLRYRVHVIPEAKA---GIIRYALGVDAFREPTALQELNTISAPSQDHVFK 316
Qy 122 VNDGFOALQGIHSLKSCIEILAAEPSTTCAGESFOVVVRNGGFRHARNVD 174
Db 317 VGN-FVALRSIORQIOEK----IFAIEGTESRSSSSFOHEMSQGFSSALSMD 364

RESULT 9
US-09-350-259-46
; Sequence 46, Application US/09350259

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Patent No. 6620915
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 6620915el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-350-259-46

Query Match 11.4%, Score 128.5, DB 4, Length 1155;
Best Local Similarity 28.9%, Pred. No. 1.2e-05;
Matches 50, Conservative 31, Mismatches 69, Indels 23, Gaps 9;

Qy 12 TLMKLTEDREQIRQGLBELOKVLPGSDPYMHGFEFASBOIYENRQGYRTA-SVYIALT 70
Db 205 TEPKSSLSPOSQSLVDAIVDQ-----GLTYTASGIQKVYKELFHSKNGARKSKAKILIVIT 259
Qy 71 DGEIHEDLFYFSE--REANRSRDIGAIYCVGVXD-FNE-TQLARI-----ADSKDHVP 121
Db 260 DQKRPDLEVRHVIPEAKA---GIIRYAGVGDAFREPALQELNLTGSAFSGDHVFK 316
Qy 122 VNDGFOALQGIITHSLKSCIEILAEPTTCAGSFQVVYVRGNGFRFARVD 174
Db 317 VGN-FVALRSIORQIOEK---IFAIBGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 10
US-08-485-618-53
Sequence 53, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-53

Query Match 11.4%, Score 128.5, DB 1, Length 1161;
Best Local Similarity 28.9%, Pred. No. 1.2e-05;
Matches 50, Conservative 31, Mismatches 69, Indels 23, Gaps 9;

Qy 12 TLMKLTEDREQIRQGLBELOKVLPGSDPYMHGFEFASBOIYENRQGYRTA-SVYIALT 70
Db 205 TEPKSSLSPOSQSLVDAIVDQ-----GLTYTASGIQKVYKELFHSKNGARKSKAKILIVIT 259
Qy 71 DGEIHEDLFYFSE--REANRSRDIGAIYCVGVXD-FNE-TQLARI-----ADSKDHVP 121
Db 260 DQKRPDLEVRHVIPEAKA---GIIRYAGVGDAFREPALQELNLTGSAFSGDHVFK 316
Qy 122 VNDGFOALQGIITHSLKSCIEILAEPTTCAGSFQVVYVRGNGFRFARVD 174
Db 317 VGN-FVALRSIORQIOEK---IFAIBGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 11
US-08-362-652-53
Sequence 53, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-53

Query Match 11.4%; Score 128.5; DB 1; Length 1161;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TLMLKTEDEIOIQLELQKVLPGGDTYHMEGPERASQIYVENRGQYRTA-SVITALT 70
Db 205 TEFKSSLSPOSIDAIYQLQ-----GLTYTASGIQYVKELFHSKNGARKSAKKILIVIT 259
Qy 71 DGEIHEDLPFYSE--REANRSRDGAIVYCVGYKD-FNE-TOLARI-----ADSKDHVP 121
Db 260 DGQKRPDLFHYRVHVPFAEKA---GIIRVAIGVDAPREPTALQELNTIGSAPSDHVF 316
Qy 122 VNDGFOLQGIHSLKSCIEIILAEPTICAGESFQVNVVRNGFPHARNVD 174
Db 317 VGN-FVALRSIORIOERK---IFAIEGTESRSSSSFOHEMSQEGFSSALSM 364

RESULT 12
US-08-605-672-53
Sequence 53, Application US/08605672
Patent No. 5817515

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:
FILING DATE: 21-DEC-1994
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-53

Query Match 11.4%; Score 128.5; DB 2; Length 1161;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TLMLKTEDEIOIQLELQKVLPGGDTYHMEGPERASQIYVENRGQYRTA-SVITALT 70
Db 205 TEFKSSLSPOSIDAIYQLQ-----GLTYTASGIQYVKELFHSKNGARKSAKKILIVIT 259
Qy 71 DGEIHEDLPFYSE--REANRSRDGAIVYCVGYKD-FNE-TOLARI-----ADSKDHVP 121
Db 260 DGQKRPDLFHYRVHVPFAEKA---GIIRVAIGVDAPREPTALQELNTIGSAPSDHVF 316
Qy 122 VNDGFOLQGIHSLKSCIEIILAEPTICAGESFQVNVVRNGFPHARNVD 174
Db 317 VGN-FVALRSIORIOERK---IFAIEGTESRSSSSFOHEMSQEGFSSALSM 364

RESULT 13
US-08-482-293A-53
Sequence 53, Application US/08482293A
Patent No. 5831029

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:
FILING DATE: 21-DEC-1994
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-53

Query Match 11.4%; Score 128.5; DB 2; Length 1161;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 13:44:26 ; Search time 21.7559 Seconds

(without alignments)
2828.659 Million cell updates/sec

Title: US-09-970-076-10

Perfect score: 1131

Sequence: 1 MSFVFSRGTTLTKLTEDR.....STSGFKGNHPCUPARHT 218

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Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:*

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Pred. No. is the number of residues predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	966	85.4	328	US-10-038-307-26	Sequence 26, App1
3	966	85.4	328	US-10-201-292-26	Sequence 26, App1
4	966	85.4	333	US-09-796-753-12	Sequence 12, App1
5	966	85.4	333	US-10-038-307-2	Sequence 2, App1
6	966	85.4	333	US-10-201-292-2	Sequence 2, App1
7	966	85.4	342	US-10-038-307-22	Sequence 22, App1
8	966	85.4	342	US-10-201-292-22	Sequence 22, App1
9	966	85.4	345	US-10-038-307-24	Sequence 24, App1
10	966	85.4	345	US-10-201-292-24	Sequence 24, App1
11	966	85.4	403	US-09-833-245-621	Sequence 621, App1
12	966	85.4	529	US-10-201-292-36	Sequence 36, App1
13	966	85.4	551	US-10-038-307-18	Sequence 18, App1
14	966	85.4	551	US-10-201-292-18	Sequence 18, App1
15	966	85.4	564	US-09-918-715-187	Sequence 187, App1

16	966	85.4	564	12	US-09-918-715-232	Sequence 232, App1
17	966	85.4	564	14	US-10-038-307-20	Sequence 20, App1
18	966	85.4	564	14	US-10-201-292-20	Sequence 20, App1
19	966	85.4	564	14	US-10-301-822-199	Sequence 199, App1
20	966	85.4	564	16	US-10-408-765A-1823	Sequence 1823, App1
21	961	85.0	403	11	US-09-833-245-620	Sequence 620, App1
22	960	84.9	562	12	US-09-918-715-194	Sequence 194, App1
23	960	84.9	562	12	US-09-918-715-301	Sequence 301, App1
24	945	83.6	534	14	US-10-038-307-12	Sequence 12, App1
25	945	83.6	534	14	US-10-201-292-12	Sequence 12, App1
26	945	83.6	543	14	US-10-038-307-10	Sequence 10, App1
27	945	83.6	543	14	US-10-038-307-14	Sequence 14, App1
28	945	83.6	543	14	US-10-038-307-16	Sequence 16, App1
29	945	83.6	543	14	US-10-201-292-10	Sequence 10, App1
30	945	83.6	543	14	US-10-201-292-14	Sequence 14, App1
31	945	83.6	543	14	US-10-201-292-16	Sequence 16, App1
32	877	77.5	479	14	US-10-201-292-32	Sequence 32, App1
33	767	67.8	460	14	US-10-201-292-28	Sequence 28, App1
34	757	66.9	460	14	US-10-201-292-30	Sequence 30, App1
35	704	62.2	538	13	US-10-047-542-99	Sequence 99, App1
36	506	44.7	245	15	US-10-094-749-2134	Sequence 2134, App1
37	506	44.7	272	15	US-10-264-237-1574	Sequence 1574, App1
38	506	44.7	488	10	US-09-796-753-52	Sequence 52, App1
39	506	44.7	488	14	US-10-038-307-6	Sequence 6, App1
40	506	44.7	488	14	US-10-201-292-6	Sequence 6, App1
41	506	44.7	488	14	US-10-368-087-16	Sequence 16, App1
42	506	44.7	488	15	US-10-104-047-2639	Sequence 2639, App1
43	505	44.7	587	9	US-09-764-870-312	Sequence 312, App1
44	505	44.7	587	11	US-09-764-875-968	Sequence 968, App1
45	505	44.7	587	14	US-10-125-540-312	Sequence 312, App1

ALIGNMENTS

RESULT 1
US-10-201-292-34
; Sequence 34, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTHMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Judith J. HEALEY
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-34

Query Match 86.4% Score 977.5, DB 14; Length 504;
Best Local Similarity 91.1% Pred. No. 8.6e-100;
Matches 194; Conservative 3; Mismatches 9; Indels 7; Gaps 1;
QY 1 MSFVFSRGTTLTKLTEDRQIRGLQVLPFGPTVMHGEPRASEQIYENRQY 60
DB 80 MSFVFSRGTTLTKLTEDRQIRGLQVLPFGPTVMHGEPRASEQIYENRQY 139
QY 61 RTASVIALTLTGELHEDLFYSEBANSRDGAIYCVGVDFNETOLARLADSKHYF 120
DB 140 RTASVIALTLTGELHEDLFYSEBANSRDGAIYCVGVDFNETOLARLADSKHYF 199
QY 121 PNDPFOALQGIHSHILKSCIEILAAPSTICAGESQVYVRGNGFPHARVNDVLCF 180
DB 200 PNDPFOALQGIHSHILKSCIEILAAPSTICAGESQVYVRGNGFPHARVNDVLCF 259
QY 181 KINDSVTLSKSLQSPWASTSGFKGNHPCUP 213

Db 260 KINDSVTLINEKPFSPKSSD-----KTHTCP 285

RESULT 2

US-10-038-307-26

/ Sequence 26, Application US/10038307

/ Publication No. US20030134786A1

/ GENERAL INFORMATION:

/ APPLICANT: James B. ROTHMAN

/ APPLICANT: Engin OZKANNAK

/ APPLICANT: Judith J. HEALEY

/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

/ FILE REFERENCE: 7853-253-999

/ CURRENT APPLICATION NUMBER: US/10/038,307

/ CURRENT FILING DATE: 2002-06-28

/ NUMBER OF SEQ ID NOS: 26

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 26

/ LENGTH: 328

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-038-307-26

Query Match 85.4%; Score 966; DB 14; Length 328;

Best Local Similarity 98.9%; Pred. No. 8,6e-99;

Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFVFSRGTTLMLKLTEDREIQGLLELQKVLPGSDTYMHGFEPRASQIYYENRQY 60

Db 80 MSFVFSRGTTLMLKLTEDREIQGLLELQKVLPGSDTYMHGFEPRASQIYYENRQY 139

Qy 61 RTASVIALTDGELHEDLPFYSEREANSRDLGAIYVCVGYKDPNETQLARIADSKHVF 120

Db 140 RTASVIALTDGELHEDLPFYSEREANSRDLGAIYVCVGYKDPNETQLARIADSKHVF 199

Qy 121 PVNDGFQALQGIHSHILKSCIEILAEPSITCAGESFQVYVVRNGGFRHANVDRVLCSP 180

Db 200 PVNDGFQALQGIHSHILKSCIEILAEPSITCAGESFQVYVVRNGGFRHANVDRVLCSP 259

Qy 181 KINDSVTLSK 190

Db 260 KINDSVTLINE 269

RESULT 3

US-10-201-292-26

/ Sequence 26, Application US/10201292

/ Publication No. US20030144193A1

/ GENERAL INFORMATION:

/ APPLICANT: James B. ROTHMAN

/ APPLICANT: Engin OZKANNAK

/ APPLICANT: Theresa L. O'KEEFE

/ APPLICANT: Judith J. HEALEY

/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

/ FILE REFERENCE: 7853-253-999

/ CURRENT APPLICATION NUMBER: US/10/201,292

/ CURRENT FILING DATE: 2003-02-14

/ NUMBER OF SEQ ID NOS: 36

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 26

/ LENGTH: 328

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-201-292-26

Query Match 85.4%; Score 966; DB 14; Length 328;

Best Local Similarity 98.9%; Pred. No. 8,6e-99;

Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFVFSRGTTLMLKLTEDREIQGLLELQKVLPGSDTYMHGFEPRASQIYYENRQY 60

Db 80 MSFVFSRGTTLMLKLTEDREIQGLLELQKVLPGSDTYMHGFEPRASQIYYENRQY 139

Qy 61 RTASVIALTDGELHEDLPFYSEREANSRDLGAIYVCVGYKDPNETQLARIADSKHVF 120

Db 140 RTASVIALTDGELHEDLPFYSEREANSRDLGAIYVCVGYKDPNETQLARIADSKHVF 199

Qy 121 PVNDGFQALQGIHSHILKSCIEILAEPSITCAGESFQVYVVRNGGFRHANVDRVLCSP 180

Db 200 PVNDGFQALQGIHSHILKSCIEILAEPSITCAGESFQVYVVRNGGFRHANVDRVLCSP 259

Qy 181 KINDSVTLSK 190

Db 260 KINDSVTLINE 269

RESULT 4

US-09-796-753-12

/ Sequence 12, Application US/09796753

/ Publication No. US20030027998A1

/ GENERAL INFORMATION:

/ APPLICANT: McCarthy, Sean A.

/ TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

/ FILE REFERENCE: 7853-227-999

/ CURRENT APPLICATION NUMBER: US/09/796,753

/ CURRENT FILING DATE: 2001-03-01

/ PRIOR APPLICATION NUMBER: 09/183,175

/ PRIOR FILING DATE: 1998-10-30

/ PRIOR APPLICATION NUMBER: 09/223,094

/ PRIOR FILING DATE: 1998-12-30

/ PRIOR APPLICATION NUMBER: 09/223,546

/ PRIOR FILING DATE: 1998-12-30

/ PRIOR APPLICATION NUMBER: 09/224,246

/ PRIOR FILING DATE: 1998-12-30

/ PRIOR APPLICATION NUMBER: 09/259,388

/ PRIOR FILING DATE: 1999-02-26

/ PRIOR APPLICATION NUMBER: 60/122,458

/ PRIOR FILING DATE: 1999-03-01

/ PRIOR APPLICATION NUMBER: 09/312,359

/ PRIOR FILING DATE: 1999-05-14

/ PRIOR APPLICATION NUMBER: 09/336,536

/ PRIOR FILING DATE: 1999-06-18

/ PRIOR APPLICATION NUMBER: 09/342,687

/ PRIOR FILING DATE: 1999-06-29

/ PRIOR APPLICATION NUMBER: 09/345,464

/ PRIOR FILING DATE: 1999-06-30

/ PRIOR APPLICATION NUMBER: 09/365,164

/ PRIOR FILING DATE: 1999-07-30

/ PRIOR APPLICATION NUMBER: 09/399,723

/ PRIOR FILING DATE: 1999-09-20

/ PRIOR APPLICATION NUMBER: 09/409,634

/ PRIOR FILING DATE: 1999-09-30

/ PRIOR APPLICATION NUMBER: 09/471,179

/ PRIOR FILING DATE: 1999-12-23

/ PRIOR APPLICATION NUMBER: 09/474,071

/ PRIOR FILING DATE: 1999-12-29

/ PRIOR APPLICATION NUMBER: 09/474,072

/ PRIOR FILING DATE: 1999-12-29

/ PRIOR APPLICATION NUMBER: 09/514,010

/ PRIOR FILING DATE: 2000-02-25

/ PRIOR APPLICATION NUMBER: 09/516,745

/ PRIOR FILING DATE: 2000-03-01

/ PRIOR APPLICATION NUMBER: 09/572,002

/ PRIOR FILING DATE: 2000-05-14

/ PRIOR APPLICATION NUMBER: 09/597,993

/ PRIOR FILING DATE: 2000-06-19

/ PRIOR APPLICATION NUMBER: 09/599,596

/ PRIOR FILING DATE: 2000-06-22

/ PRIOR APPLICATION NUMBER: 09/630,334

/ PRIOR FILING DATE: 2000-07-31

/ PRIOR APPLICATION NUMBER: 09/606,565

/ PRIOR FILING DATE: 2000-06-29

/ PRIOR APPLICATION NUMBER: 09/606,317

/ PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: 09/665,666
 PRIOR FILING DATE: 2000-09-20
 PRIOR APPLICATION NUMBER: 09/677,751
 PRIOR FILING DATE: 2000-09-30
 NUMBER OF SEQ ID NOS: 162
 SEQ ID NO 12
 LENGTH: 333
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-796-753-12

Query Match 85.4%; Score 966; DB 10; Length 333;
 Best Local Similarity 98.9%; Pred. No. 8.8e-99;
 Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREQIRQGLELQKVLPGGDTYMHGFERASEQIYYENRQY 60
 DB 80 MSFVFSRGTTLMLKLTEDREQIRQGLELQKVLPGGDTYMHGFERASEQIYYENRQY 139
 QY 61 RTASVIALTDLGELHEDLFFYSEREANRSRDIGALVYCVGVDFNETQIARIADSKDHF 120
 DB 140 RTASVIALTDLGELHEDLFFYSEREANRSRDIGALVYCVGVDFNETQIARIADSKDHF 199
 QY 121 PVNDGFOALQGIHHSILKSCIEIILAEPSITCAGESFOVVVRGNGFPHARVNDVLCSE 180
 DB 200 PVNDGFOALQGIHHSILKSCIEIILAEPSITCAGESFOVVVRGNGFPHARVNDVLCSE 259
 QY 181 KINDSVTLSK 190
 DB 260 KINDSVTLINE 269

RESULT 5

US-10-038-307-2
 Sequence 2, Application US/10038307
 Publication No. US20030134786A1
 GENERAL INFORMATION:
 APPLICANT: James B. ROTTMAN
 APPLICANT: Theresa L. O'KEEFE
 APPLICANT: Engin OZKAYNAK
 APPLICANT: Judith J. HEALEY
 TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
 FILE REFERENCE: 7853-253-999
 CURRENT APPLICATION NUMBER: US/10/038,307
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 333
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-038-307-2

Query Match 85.4%; Score 966; DB 14; Length 333;
 Best Local Similarity 98.9%; Pred. No. 8.8e-99;
 Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREQIRQGLELQKVLPGGDTYMHGFERASEQIYYENRQY 60
 DB 80 MSFVFSRGTTLMLKLTEDREQIRQGLELQKVLPGGDTYMHGFERASEQIYYENRQY 139
 QY 61 RTASVIALTDLGELHEDLFFYSEREANRSRDIGALVYCVGVDFNETQIARIADSKDHF 120
 DB 140 RTASVIALTDLGELHEDLFFYSEREANRSRDIGALVYCVGVDFNETQIARIADSKDHF 199
 QY 121 PVNDGFOALQGIHHSILKSCIEIILAEPSITCAGESFOVVVRGNGFPHARVNDVLCSE 180
 DB 200 PVNDGFOALQGIHHSILKSCIEIILAEPSITCAGESFOVVVRGNGFPHARVNDVLCSE 259
 QY 181 KINDSVTLSK 190
 DB 260 KINDSVTLINE 269

RESULT 6

US-10-201-292-2
 Sequence 2, Application US/10201292
 Publication No. US20030144193A1
 GENERAL INFORMATION:
 APPLICANT: James B. ROTTMAN
 APPLICANT: Theresa L. O'KEEFE
 APPLICANT: Engin OZKAYNAK
 APPLICANT: Judith J. HEALEY
 TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
 FILE REFERENCE: 7853-253-999
 CURRENT APPLICATION NUMBER: US/10/201,292
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 333
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-201-292-2

Query Match 85.4%; Score 966; DB 14; Length 333;
 Best Local Similarity 98.9%; Pred. No. 8.8e-99;
 Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREQIRQGLELQKVLPGGDTYMHGFERASEQIYYENRQY 60
 DB 80 MSFVFSRGTTLMLKLTEDREQIRQGLELQKVLPGGDTYMHGFERASEQIYYENRQY 139
 QY 61 RTASVIALTDLGELHEDLFFYSEREANRSRDIGALVYCVGVDFNETQIARIADSKDHF 120
 DB 140 RTASVIALTDLGELHEDLFFYSEREANRSRDIGALVYCVGVDFNETQIARIADSKDHF 199
 QY 121 PVNDGFOALQGIHHSILKSCIEIILAEPSITCAGESFOVVVRGNGFPHARVNDVLCSE 180
 DB 200 PVNDGFOALQGIHHSILKSCIEIILAEPSITCAGESFOVVVRGNGFPHARVNDVLCSE 259
 QY 181 KINDSVTLSK 190
 DB 260 KINDSVTLINE 269

RESULT 7

US-10-038-307-22
 Sequence 22, Application US/10038307
 Publication No. US20030134786A1
 GENERAL INFORMATION:
 APPLICANT: James B. ROTTMAN
 APPLICANT: Theresa L. O'KEEFE
 APPLICANT: Engin OZKAYNAK
 APPLICANT: Judith J. HEALEY
 TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
 FILE REFERENCE: 7853-253-999
 CURRENT APPLICATION NUMBER: US/10/038,307
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 22
 LENGTH: 342
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-038-307-22

Query Match 85.4%; Score 966; DB 14; Length 342;
 Best Local Similarity 98.9%; Pred. No. 9.2e-99;
 Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREQIRQGLELQKVLPGGDTYMHGFERASEQIYYENRQY 60
 DB 89 MSFVFSRGTTLMLKLTEDREQIRQGLELQKVLPGGDTYMHGFERASEQIYYENRQY 148
 QY 61 RTASVIALTDLGELHEDLFFYSEREANRSRDIGALVYCVGVDFNETQIARIADSKDHF 120

```
Db 149 RTASVITLTDGELHEDLFFYSEREANRSRDIGAIYVCVGDYMHGFEFASQIYYENRQGY 208
Qy 121 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVRNGGFRHARNVDRVLCSE 180
Db 209 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVRNGGFRHARNVDRVLCSE 268
Qy 181 KINDSVTLSK 190
Db 269 KINDSVTLINE 278
```

RESULT 8

```
US-10-201-292-22
; Sequence 22, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-22
```

```
Query Match 85.4%; Score 966; DB 14; Length 342;
Best Local Similarity 98.9%; Pred. No. 9,2e-99;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFEFASQIYYENRQGY 60
Db 89 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFEFASQIYYENRQGY 148
Qy 61 RTASVITLTDGELHEDLFFYSEREANRSRDIGAIYVCVGDYMHGFEFASQIYYENRQGY 120
Db 149 RTASVITLTDGELHEDLFFYSEREANRSRDIGAIYVCVGDYMHGFEFASQIYYENRQGY 208
Qy 121 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVRNGGFRHARNVDRVLCSE 180
Db 209 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVRNGGFRHARNVDRVLCSE 268
Qy 181 KINDSVTLSK 190
Db 269 KINDSVTLINE 278
```

RESULT 9

```
US-10-038-307-24
; Sequence 24, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-10-038-307-24

```
Query Match 85.4%; Score 966; DB 14; Length 345;
Best Local Similarity 98.9%; Pred. No. 9,3e-99;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFEFASQIYYENRQGY 60
Db 80 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFEFASQIYYENRQGY 139
Qy 61 RTASVITLTDGELHEDLFFYSEREANRSRDIGAIYVCVGDYMHGFEFASQIYYENRQGY 120
Db 140 RTASVITLTDGELHEDLFFYSEREANRSRDIGAIYVCVGDYMHGFEFASQIYYENRQGY 199
Qy 121 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVRNGGFRHARNVDRVLCSE 180
Db 200 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVRNGGFRHARNVDRVLCSE 259
Qy 181 KINDSVTLSK 190
Db 260 KINDSVTLINE 269
```

RESULT 10

```
US-10-201-292-24
; Sequence 24, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-24
```

```
Query Match 85.4%; Score 966; DB 14; Length 345;
Best Local Similarity 98.9%; Pred. No. 9,3e-99;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFEFASQIYYENRQGY 60
Db 80 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFEFASQIYYENRQGY 139
Qy 61 RTASVITLTDGELHEDLFFYSEREANRSRDIGAIYVCVGDYMHGFEFASQIYYENRQGY 120
Db 140 RTASVITLTDGELHEDLFFYSEREANRSRDIGAIYVCVGDYMHGFEFASQIYYENRQGY 199
Qy 121 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVRNGGFRHARNVDRVLCSE 180
Db 200 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFOVVVRNGGFRHARNVDRVLCSE 259
Qy 181 KINDSVTLSK 190
Db 260 KINDSVTLINE 269
```

RESULT 11

```
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
```


CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 621
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-621

Query Match 85.4%; Score 966; DB 11; Length 403;
Best Local Similarity 98.9%; Pred. No. 1.2e-98;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREIQGLLEQVLPFGDTVMHEGPERASEQIYYENRQGY 60
DB 80 MSFVFSRGTTLMLKLTEDREIQGLLEQVLPFGDTVMHEGPERASEQIYYENRQGY 139
QY 61 RTASVITALTDELHEDLFFYSERBANSRDLGAIYVCVGVKDFNETOLARIADSKDHF 120
DB 140 RTASVITALTDELHEDLFFYSERBANSRDLGAIYVCVGVKDFNETOLARIADSKDHF 199
QY 121 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRGNGFPHARVNDVRLCSF 180
DB 200 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRGNGFPHARVNDVRLCSF 259
QY 181 KINDSVTLTK 190
DB 260 KINDSVTLTK 269

RESULT 12
US-10-201-292-36
Sequence 36, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 36
LENGTH: 529
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-36

Query Match 85.4%; Score 966; DB 14; Length 529;
Best Local Similarity 98.9%; Pred. No. 1.8e-98;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREIQGLLEQVLPFGDTVMHEGPERASEQIYYENRQGY 60
DB 80 MSFVFSRGTTLMLKLTEDREIQGLLEQVLPFGDTVMHEGPERASEQIYYENRQGY 139
QY 61 RTASVITALTDELHEDLFFYSERBANSRDLGAIYVCVGVKDFNETOLARIADSKDHF 120
DB 140 RTASVITALTDELHEDLFFYSERBANSRDLGAIYVCVGVKDFNETOLARIADSKDHF 199
QY 121 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRGNGFPHARVNDVRLCSF 180
DB 200 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRGNGFPHARVNDVRLCSF 259

QY 181 KINDSVTLTK 190
DB 260 KINDSVTLTK 269

RESULT 13
US-10-038-307-18
Sequence 18, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 18
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-18

Query Match 85.4%; Score 966; DB 14; Length 551;
Best Local Similarity 98.9%; Pred. No. 1.9e-98;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREIQGLLEQVLPFGDTVMHEGPERASEQIYYENRQGY 60
DB 80 MSFVFSRGTTLMLKLTEDREIQGLLEQVLPFGDTVMHEGPERASEQIYYENRQGY 139
QY 61 RTASVITALTDELHEDLFFYSERBANSRDLGAIYVCVGVKDFNETOLARIADSKDHF 120
DB 140 RTASVITALTDELHEDLFFYSERBANSRDLGAIYVCVGVKDFNETOLARIADSKDHF 199
QY 121 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRGNGFPHARVNDVRLCSF 180
DB 200 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRGNGFPHARVNDVRLCSF 259
QY 181 KINDSVTLTK 190
DB 260 KINDSVTLTK 269

RESULT 14
US-10-201-292-18
Sequence 18, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 18
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-18

Query Match 85.4%; Score 966; DB 14; Length 551;
Best Local Similarity 98.9%; Pred. No. 1.9e-98;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	MSLIVSTRGCTLMKLTEDREQLROGLSELOKVLGGGTYHHEGERSASEQIYENKQY 60
Db	MSLIVSTRGCTLMKLTEDREQLROGLSELOKVLGGGTYHHEGERSASEQIYENKQY 139
Qy	RTASVLIATLDELHEDLFFYSERENRSGDGAIVYCVGKDFNETOLARIADSKDHF 120
Db	RTASVLIATLDELHEDLFFYSERENRSGDGAIVYCVGKDFNETOLARIADSKDHF 199
Qy	PVNDGFOALOGIIHSLILKKSCEIILAESTTCAGESQVYVYVNGRFRHARNDRVLCSP 180
Db	PVNDGFOALOGIIHSLILKKSCEIILAESTTCAGESQVYVYVNGRFRHARNDRVLCSP 259
Qy	KINDSVTLSK 190
Db	KINDSVTLNE 269

```

RESULT 15 715-187
; Sequence 187, Application US/09/918715
; Publication No. US2003001157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107, 00134
; CURRENT APPLICATION NUMBER: US/09/918, 715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,559
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-918-715-187

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Query Match	85.4%	Score 966	DB 12	Length 564
Best Local Similarity	98.9%	Pred. No. 1.9e-98		
Matches 188	Conservative	2	Mismatches 0	Indels 0
			Gaps	0

Qy	MSFVFESTRGTTLTKLTLEBEOIROLLELOKVLGSGPTVMEGPERASBOIYYENKQY 60
Db	MSFVFESTRGTTLTKLTLEBEOIROLLELOKVLGSGPTVMEGPERASBOIYYENKQY 139
Qy	RTASVVIATLDGELHEDLPFYSERENRSDIGAIYVCVGDVFNETOLARIADSKOHV 120
Db	RTASVVIATLDGELHEDLPFYSERENRSDIGAIYVCVGDVFNETOLARIADSKOHV 139
Qy	PVNDGFQALGGIIHSLIKKSCIEIILAEPSTCAGESFQVYVVRNGGFRHADVRLCSF 180
Db	PVNDGFQALGGIIHSLIKKSCIEIILAEPSTCAGESFQVYVVRNGGFRHADVRLCSF 259
Qy	181 KINDSVTLSK 190
Db	260 KINDSVTLNE 269

Search completed: June 21, 2004, 14:02:14
Job time : 21.7559 Secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 22, 2004, 02:37:46 ; Search time 496.02 Seconds
(without alignments)
3075.489 Million cell updates/sec

Title: US-09-970-076-8

Perfect score: 1728

Sequence: 1 MATERRALGIGFQWLSLST.....TTTCSLHKIAAGPTTAACME 333

Scoring table:

BLOSUM62		
Xgapop 10.0 ,	Xgapext 0.5	
Ygapop 10.0 ,	Ygapext 0.5	
Fgapop 6.0 ,	Fgapext 7.0	
Delop 6.0 ,	Delext 7.0	

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO.apool/US09970076/runac_21062004_125533_8805/app_query.fasta_1.2140
-DB=Published Applications NA -GEMT=fastcap -SUFFIX=rmph -MINMATCH=0.1
-LOOPT=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076@cgn2_1.1.1225@runac_21062004_125533_8805
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -TRENDS=1 -XGAPEXT=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTOS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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1	1728	100.0	1713	15	US-10-038-307-19	Sequence 19, Appl
2	1728	100.0	1712	15	US-10-201-292-19	Sequence 19, Appl
3	1728	100.0	2272	15	US-09-796-753-11	Sequence 11, Appl
4	1728	100.0	2272	15	US-10-038-307-1	Sequence 1, Appl
5	1728	100.0	2272	15	US-10-201-292-1	Sequence 1, Appl
6	1728	100.0	2353	15	US-10-198-846-9957	Sequence 9957, Ap
7	1728	100.0	2459	9	US-09-833-381-998	Sequence 998, App
8	1718	99.4	1056	15	US-10-038-307-23	Sequence 23, Appl
9	1718	99.4	1056	15	US-10-201-292-23	Sequence 23, Appl
10	1713.5	99.2	1047	15	US-10-038-307-21	Sequence 21, Appl
11	1713.5	99.2	1047	15	US-10-201-292-21	Sequence 21, Appl
12	1650.5	95.5	1674	15	US-10-038-307-17	Sequence 17, Appl
13	1650.5	95.5	1674	15	US-10-201-292-17	Sequence 17, Appl
14	1649	95.4	1454	16	US-10-133-537-58	Sequence 58, Appl
15	1649	95.4	1454	16	US-10-159-563-58	Sequence 58, Appl
16	1649	95.4	1650	15	US-10-038-307-13	Sequence 13, Appl
17	1649	95.4	1650	15	US-10-038-307-15	Sequence 15, Appl
18	1649	95.4	1650	15	US-10-201-292-13	Sequence 13, Appl
19	1649	95.4	1650	15	US-10-201-292-15	Sequence 15, Appl
20	1649	95.4	5540	13	US-09-918-715-176	Sequence 176, App
21	1649	95.4	5540	13	US-09-918-715-231	Sequence 231, App
22	1649	95.4	5540	15	US-10-301-822-198	Sequence 198, App
23	1639	94.8	1650	15	US-10-038-307-9	Sequence 9, Appl
24	1639	94.8	1650	15	US-10-201-292-9	Sequence 9, Appl
25	1636	94.7	1008	15	US-10-038-307-25	Sequence 25, Appl
26	1636	94.7	1008	15	US-10-201-292-25	Sequence 25, Appl
27	1599	92.5	2397	16	US-10-062-674-1757	Sequence 1757, Ap
28	1556	90.0	1608	15	US-10-201-292-35	Sequence 35, Appl
29	1553	89.9	5220	13	US-09-918-715-186	Sequence 186, App
30	1553	89.9	5220	13	US-09-918-715-300	Sequence 300, App
31	1508	87.3	1623	15	US-10-038-307-11	Sequence 11, Appl
32	1508	87.3	1623	15	US-10-201-292-11	Sequence 11, Appl
33	1423	82.3	1534	15	US-10-201-292-33	Sequence 33, Appl
34	1392	80.6	1609	15	US-10-037-270-8	Sequence 8, Appl
35	1392	80.6	1609	16	US-10-117-122-8	Sequence 8, Appl
36	1313	76.0	1464	15	US-10-201-292-31	Sequence 31, Appl
37	1193	69.0	1401	15	US-10-201-292-27	Sequence 27, Appl
38	1193	69.0	1401	15	US-10-201-292-27	Sequence 27, Appl
39	903	52.3	1650	14	US-10-047-542-98	Sequence 98, Appl
40	903	52.3	6602	14	US-10-047-542-100	Sequence 100, App
41	800.5	46.3	2234	16	US-10-104-047-669	Sequence 669, App
42	800.5	46.3	3677	10	US-09-796-753-51	Sequence 51, Appl
43	800.5	46.3	3677	15	US-10-038-307-5	Sequence 5, Appl
44	800.5	46.3	3677	15	US-10-201-292-5	Sequence 5, Appl
45	800.5	46.3	4081	15	US-10-368-087-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-10-038-307-19
; Sequence 19, Application US/10038307
; Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTHMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OKYAKMAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 1713
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-19
Alignment Scores: 7.08e-220 Length: 1713
Pred. No.: 1713

QY 201 ValaanaapgyphglnalaleuenglylleilehiserlleleuylaylserserCys 220
DB 613 GTGAATGAGCGGCTTTCAGGCTTGCAGGCACTCATCTCAATTTGAGAAAGCTCTGC 672
QY 221 lileguilleleuvalaleuuproserthrilleybalaaglyluserphglnalval 240
DB 673 ATCGAAATTTCTAGAGCTGACCACTCCATCCATATGCGAGAGCTTCAATTGCTTC 732
QY 241 Valaaggyaenglylphglnalaleuenglyluserphglnalvalaleuylaylserser 260
DB 733 GTGAAGAGGAAACGGCTTCCGACATGCCCAAGCTGACAGGCTCTGCGAGCTTCAAG 792
QY 261 lileanaapservalthrlleuenglyluserphglnalaleuylaylserserthrlleu 280
DB 793 ATCAATGACTCGCTCATCATATGAGAGCGCTTCTGAGAAATCTTATTACG 852
QY 281 Cysproalaproilleuenglyluserphglnalaleuylaylserserthrlleu 300
DB 853 TGTCCAGCGGCTTTCATTAAGAGCTGCAAGAGCTGCAAGCTGCAAGCTGCAAG 912
QY 301 lileguilleleuvalaleuenglyluserphglnalaleuylaylserserthrlleu 320
DB 913 GATGCGCTCTCTTATCTCCAGTCTGTCATCATCACACACACAGTGTAGCTTCAC 972
QY 321 lileuileaserglylprothrlleuenglyluserphglnalaleuylaylserser 333
DB 973 AAAATTGATCAGGCGCCCAACAGCTGCTGATGAGAA 1011

RESULT 3

US-09-796-753-11

Sequence 11, Application US/09796753

Publication No. US20030027998A1

GENERAL INFORMATION:

APPLICANT: McCarthy, Sean A.

TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

FILE REFERENCE: 7853-227-999

CURRENT APPLICATION NUMBER: US/09/796,753

PRIOR FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 09/183,175

PRIOR FILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: 09/223,094

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/223,546

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/224,246

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/259,388

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/122,458

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: 09/312,359

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 09/336,536

PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 09/342,687

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 09/345,464

PRIOR FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: 09/365,164

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/399,723

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 09/409,634

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 09/471,179

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 09/474,071

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/474,072

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/514,010

PRIOR FILING DATE: 2000-02-25

PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 11
LENGTH: 2272
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (213)...(1211)
US-09-796-753-11

Alignment Scores:

Pred. No.:	1,136-219	Length:	2272
Score:	1728.00	Matches:	333
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-970-076-8 (1-333) x US-09-796-753-11 (1-2272)

QY 1 Metalaatrhalagluarargalaleuenglylleiglyphglntrpmluserleuathr 20
DB 213 ATGGCAGCGGCGGAGCGAGGCGCTCGGCACTCGGCTTCCAGTGGCTCTTTCGCACT 272
QY 21 LeuValleuileCysAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTyr 40
DB 273 CTGGTCTCATCTGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 332
QY 41 GlyGlyPheAspLeuTyrPheIleuAspLysSerGlySerValLeuHisIleTrpAsn 60
DB 333 GCGGATTTGACCTTCACTTATTTGACCAATCAGGAAGTGTCTGACCACTGGAAT 392
QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
DB 393 GAAATCTTATCTTGTGGAACAGTGGCTCAAAATTCATCAGCCCAAGTGAAGATG 452
QY 81 SerPheIleValPheSerThrArgGlyThrThrlleuMetLysLeuThrlleuAspArgGlu 100
DB 453 TCTTATTTGTTTCTTCCACCGAGAGAACCTTAATGAACCTAAGAGAGAGAGAGAG 512
QY 101 GlnIleArgGlnGlyLeuGluGluGlnLysValLeuProGlyGlyAspThrTyrMet 120
DB 513 CAATCCCTCAAGGCTGAGAGAACTCCAGAAAGTTCGCGAGAGAGAGAGAGAGAGAG 572
QY 121 HisGlyLysPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
DB 573 CATGAGAGATTTGAAAGGCGGAGGAGAGAGATTTTATGAAACAGAGAGAGAGAGAG 632
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisLysAspLeuPhePheTyr 160
DB 633 ACAGCCAGGCTCATATGCTTTCATGACATGAGAGAGAGAGAGAGAGAGAGAGAGAG 692
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
DB 693 TCAG 752

Qy 181 LysAspPheAenGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db 753 AAAAGTTTCATGAGACACAGCTGGCCGGATGGCGACATGTAAGCATGTGTTCCC 812
Qy 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db 813 GTGATGACGGCTCTTCAAGCTCTCGAAGCATCATCACTCAATTTTGAGAGAGCTTGC 872
Qy 221 ILeGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyIleSerPheGlnValVal 240
Db 873 ATCGAAATTTCTAGCAGCTGACATCCACATATGTGAGAGAGACTCATTTCAAGTTGTC 932
Qy 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValIleuCySerPheLys 260
Db 933 GTGAGAGGAACGGCTTCGACATCCCGCAACGTGACAGGCTCTTCGACGCTTCAG 992
Qy 261 ILeAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyLeuLeu 280
Db 993 ATCAATGACTCGGTCACTCAATAGAGAACCTTTCTGTGGAAGATACTTATTACTG 1052
Qy 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db 1053 TGTCCAGCGCTTATCTTAAAGAGTTGACATGAAGGCTGCACTCCAGGTGACATGAA 1112
Qy 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCySerLeuHis 320
Db 1113 GATGCCCTCTCTTTATCTCCAGTTCTGTGATCATCACACACACACATGTAGCTCCAC 1172
Qy 321 LysIleAlaSerGlyProThrThrAlaAlaCyMetGlu 333
Db 1173 AAAATTGCATCAGGCCCAACAGCTGCTTCATGAGAA 1211

RESULT 4
US-10-038-307-1
; Sequence 1, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2272
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213) ... (1211)
US-10-038-307-1

Alignment Scores:
Pred. No.: 1,13e-219 Length: 2272
Score: 1728.00 Matches: 333
Percent Similarity: 100.00% Conservative: 333
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-8 (1-333) x US-10-038-307-1 (1-2272)

Qy 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db 213 ATGGCAGCGCGGAGAGGAGGCTCGGCACTGGCTTCAGTGGCTCTCTTGGCCACT 272
Qy 21 LeuValIleuLleCyAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCySerTy 40

Db 273 CTGGTGTCTATCTGGCCGGGCAAGGGGAGCGAGGAGGATGGGGGTCCAGCTGCTAC 332
Qy 41 GlyIlePheAspLeuTyThrPheIleLeuAspLysSerGlySerValIleuHisIleTrpAsn 60
Db 333 GCGGATTTTAACTGTACTTCTATTTTGGACAAATGACGAAAGTGTGCTGCACACTGGAA 392
Qy 61 GluIleTyThrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
Db 393 GAATCTATTACTTGTGGAACAGTTGGCTCACAAATTCATACAGCCACAGTTAGAAATG 452
Qy 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db 453 TCTTTATGTGTCTCCACCCGAGGAACCTTAATGAACTGAGAAAGAGAGAGAA 512
Qy 101 GlnIleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyIleAspThrTyMet 120
Db 513 CAATCCGTCAAGGCTTGAAGAACTCCAGAACTTCCAGAGAGAGACACTTACATG 572
Qy 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyTyGluAsnArgGlnTyArg 140
Db 573 CATGAAGATTTGAAAGGCGCAGTGAAGATTTATTATGAAACAGACAAAGGTTACAG 632
Qy 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 160
Db 633 ACAGCCAGCGTCATCATTTGCTGACATGAGAGAACTCCATGAAATCTCTTTTCTAT 692
Qy 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyCysValGlyVal 180
Db 693 TCAAGAGGAGGCTTATAGGTCTCGAGATCTTGTCATTTGTTACTGTGTGGTGTG 752
Qy 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db 753 AAAGATTTTCATGAGACACAGCTGGCCGGATTTGCGGACATGATGATCATGTGTTCCC 812
Qy 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db 813 GTGATGACGGCTTCTTCAAGCTCTGCAAGCATCATCACTCAATTTTGAGAGAGCTTGC 872
Qy 221 ILeGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyIleSerPheGlnValVal 240
Db 873 ATCGAAATTTCTAGCAGCTGACATCCACATATGTGACAGAGTCACTTCAAGTTGTC 932
Qy 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValIleuCySerPheLys 260
Db 933 GTGAGAGGAACGGCTTCGACATCCCGCAACGTGACAGGCTCTTCGACGCTTCAG 992
Qy 261 ILeAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyLeuLeu 280
Db 993 ATCAATGACTCGGTCACTCAATAGAGAACCTTTCTGTGGAAGATACTTATTACTG 1052
Qy 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db 1053 TGTCCAGCGCTTATCTTAAAGAGTTGACATGAAGGCTGCACTCCAGGTGACATGAA 1112
Qy 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCySerLeuHis 320
Db 1113 GATGCCCTCTCTTTATCTCCAGTTCTGTGATCATCACACACACACATGTAGCTCCAC 1172
Qy 321 LysIleAlaSerGlyProThrThrAlaAlaCyMetGlu 333
Db 1173 AAAATTGCATCAGGCCCAACAGCTGCTTCATGAGAA 1211

RESULT 5
US-10-201-292-1
; Sequence 1, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999

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/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 2272
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (213)...(1211)
US-10-201-292-1

Alignment Scores:
Pred. No.: 1,136-219 Length: 2272
Score: 1728.00 Matches: 333
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-8 (1-333) x US-10-201-292-1 (1-2272)

Qy 1 MetAlaThraAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db 213 ATGGCAGCGGCGAGGAGGAGCCCTCGGCATCGGCTTCAAGTGGCTCTTTGGCCACT 272
Qy 21 LeuValLeuIleCyAlaGlyGlnGlyGlyArgArgGlyGlyProAlaCySerTy 40
Db 273 CTGGGCTCATCTGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 332
Qy 41 GlyGlyPheAspLeuTyPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db 333 GCGGATTTGACCTGACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 392
Qy 61 GluIleTyTyPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
Db 393 GAAATCTATTACTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGATG 452
Qy 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db 453 TCCCTTATTGTTTCTCCACCCGAGGAAACACCTTAAATGAACTGACAGAAACAGAA 512
Qy 101 GlnIleArgGlnGlyLeuGlnGlyLeuGlnLysValLeuProGlyGlyAspThrTyMet 120
Db 513 CAATTCCTGCAAGGCTTGAAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATG 572
Qy 121 HisGlnGlyPheGluArgLysSerGlnIleTyTyTyGluAspArgGlnGlyTyArg 140
Db 573 CATGAAGGATTTGAAAGGCGCAGTGAAGATTTATATGAAACAGACAGAGTACAGG 632
Qy 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGlnAspLeuPhePheTy 160
Db 633 ACAGCCAGGCTCATCTGCTTGAATGATGAGAACTCCAGAAAGATCTTTTCTAT 692
Qy 161 SerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTyCySerValGlyAl 180
Db 693 TCAGAGAGGAGGCTAAATAGTCTGAGATCTTGGCAATGTTTACCTGCTGCTGAG 752
Qy 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db 753 AAAGATTTCAATGAGACACAGCTGCGCGGATTTGGGACAGTAAAGATCATGTGTTCC 812
Qy 201 ValAspAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCyS 220
Db 813 GTGAATGACGCGCTTCAAGGCTTGCAGAGGATCATCTCAATTTTGAAGAGCTTCGC 872
Qy 221 IleGluIleLeuAlaGluProSerThrIleCyAlaGlyGlySerPheGlnValVal 240
Db 873 ATCGAAATTTCAAGAGCTGAAACATCCACATATGTCAGAGAGATCATTTAAATTCG 932
Qy 241 ValArgGlyAsnGlyPheArgHisAlaAspAsnValAspArgValLeuCySerPheLys 260

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Db 933 GTGAGAGAAACGCGCTTCCGACATGCCCGCAACGTGACAGAGTCTCTGACGCTTCAAG 992
Qy 261 IleAspAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyLeuLeu 280
Db 993 ATCAATGACTGCTGACACTCAATGAGAAAGCCCTTTCTGTGAGAGATCTTATTACTG 1052
Qy 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db 1053 TGTCAAGGCTCATCTTAAAGAAAGTTGGCATGAAAGCTGCATCCAGCTCAGCATGAAAC 1112
Qy 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrHisCySerLeuHis 320
Db 1113 GATGCGCTCTCTTTATCTCCAGTTCGTCTCATATCAACACACACTGATGACTTCAC 1172
Qy 321 LysIleAlaSerGlyProThrThrAlaAlaCysMetGlu 333
Db 1173 AAATTCATCAGGCGCCCAACAGCTGTTCATGAA 1211

RESULT 6
US-10-198-846-9957
/ Sequence 9957, Application US/10198846
/ Publication No. US20030099974A1
/ GENERAL INFORMATION:
/ APPLICANT: Lillie, James
/ APPLICANT: Xu, Yongyao
/ APPLICANT: Wang, Youzhen
/ APPLICANT: Steinhann, Kathleen
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
/ TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ FILE REFERENCE: MRI-049
/ CURRENT APPLICATION NUMBER: US/10/198,846
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/306,220
/ NUMBER OF SEQ ID NOS: 14084
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9957
/ LENGTH: 2353
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1, 2_2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351,
/ OTHER INFORMATION: n = A,T,C or G
US-10-198-846-9957

Alignment Scores:
Pred. No.: 1,26-219 Length: 2353
Score: 1728.00 Matches: 333
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-8 (1-333) x US-10-198-846-9957 (1-2353)

Qy 1 MetAlaThraAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db 294 ATGGCAGCGGCGAGGAGGAGCCCTCGGCATCGGCTTCAAGTGGCTCTTTGGCCACT 353
Qy 21 LeuValLeuIleCyAlaGlyGlnGlyGlyArgArgGlyGlyProAlaCySerTy 40
Db 354 CTGGGCTCATCTGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 413
Qy 41 GlyGlyPheAspLeuTyPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db 414 GCGGATTTGACCTGACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 473
Qy 61 GluIleTyTyPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
Db 474 GAAATCTATTACTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGATG 533

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QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db TCCTTATTGTTTCTCCACCGAGAGAACCTTAATGAACTGACAGAAAGACAGAGAA 593
QY 101 GlnIleArgGlnGlyLeuGlnGlyLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db CAATCCCTCAAGGCTTGAAGAACTCCAGAAAGTTCTCCAGAGGAGACACTTACATG 653
QY 121 HisGlnGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
Db CATGAGGATTTGAAAGGCCGAGTACGAGATTTTATGAAACAGCAAGGATACAGG 713
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160
Db AAGCCACGTCATCATGCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 773
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db TCAGAGAGGAGGCTAAATGATGCTCGAGATCTTGTCATTTGTTTACTGTGTGTGTG 833
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db AAAGATTCAATGACACACAGCTGCGCCGAGTTGCGACAGTAAAGATCATGTGTTTCC 893
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db GTGAATGACGGCTTCAAGCTCTGCAAGCATCATCACTCAATTTTGAAGAGTCTGCG 953
QY 221 IleGluIleLeuAlaIleGluProSerThrIleCysValGlyGluSerPheGlnValVal 240
Db ATCGAAATTTCAAGCAGCTGAACCATCCACATATGTGAGAGAGTCAATTTCAAGTTGTC 1013
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAlaAspArgValLeuCysSerPheLys 260
Db GTGAGAGAAACGGCTTCCGACATCCCGCAACGTGACAGGCTCTTGCAGCTTCAAG 1073
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
Db ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAAAGATATTATTACTG 1133
QY 281 CysProAlaProIleLeuLysGlyValGlyMetLysValAlaLeuGlnValSerMetAsn 300
Db TGTCACAGGCGCTTATCTTAAAGAACTGGCATGAAGCTGCATCCAGGTACGATGAAC 1193
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerLeuHis 320
Db GATGCTCTCTTTTATCTCCAGTTCTGTCTCATCATACACACACACTGTAAGCTCCAC 1253
QY 321 LysIleAlaSerGlyProThrThrAlaAlaCysMetGlu 333
Db 1254 AAAATTGCATCAGGCCCAACACAGCTGCTTGATGAGA 1292

RESULT 7
US-09-833-381-998
; Sequence 998, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 998
; LENGTH: 2459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1)...(2459)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-998

Alignment Scores:
Pred. No.: 1,296-219 Length: 2459
Score: 1728.00 Matches: 333
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-970-076-8 (1-333) x US-09-833-381-998 (1-2459)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnThrLeuSerLeuAlaThr 20
Db ATGGCCACGGCGGAGCGGAGAGCCCTCGCATCGGCTTCCAGTGGCTCTTTGGCACT 471
QY 21 LeuValLeuIleCysAlaGlyGlnGlyIleArgArgGluAspGlyIleProAlaCysTyr 40
Db CTGGTGCTCATCTGCGCGGGCAAGGGGAGCGCAGGAGGATGGGGGTCCAGCTGCTAC 531
QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHisIleTyrAsn 60
Db GCGGATTTGACCTGTACTTCAATTTTGACAAATCAGAAAGTGTGTGCACCACTGAAT 591
QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
Db GAATCTTATTTCTTGTGGAACAGTTGGCTCACAAATTCATACGCCACAGTTGAGAAAG 651
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db TCCTTATTGTTTCTCCACCGAGAAACAACCTTAATGAACATGACAGAAAGACAGAGAA 711
QY 101 GlnIleArgGlnGlyLeuGlnGlyLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db CAATCCGTCAGAGCTTGAAGAACTCCAGAAAGTTGTGACAGAGAGACACTTAACATG 771
QY 121 HisGlnGlyPheGluArgAlaSerGluGlnIleTyrTyrGlnAsnArgGlnGlyTyrArg 140
Db CATGAAGATTTGAAAGGCCGACGTGACAGATTTATTTATGAAACACACAGGCTTACAG 831
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheTyr 160
Db ACAGCCAGCTCATCATTTGCTTGACATGATGAGAACTCCATGAAGATCTCTTTTCTAT 891
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db TCAGAGAGGAGGCTAAATGAGTCTCGAGATCTGTGTCAATGTGTTACTGTGTGTGTG 951
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db AAAGATTTCATGACACACAGCTGCGCCGAGATTCGGAACGTAAAGATCATGTGTTCCC 1011
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db GTGAATGACGGCTTCAAGCTCTGCAAGGATCATCACTCAATTTTGAAGAAAGTCTCTGC 1071
QY 221 IleGluIleLeuAlaIleGluProSerThrIleCysValGlyGluSerPheGlnValVal 240
Db ATCGAAATTTCAAGAGCTGAACCATCCACATATGTGACAGAGAGTCAATTTCAAGTTGTC 1131
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAlaAspArgValLeuCysSerPheLys 260
Db GTGAGAGAAACGGCTTCCACATGCGCCGACAGTGAACAGGCTCTCTGACGTTCAAG 1191
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
Db ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAAAGATATTATTACTG 1251
QY 281 CysProAlaProIleLeuLysGlyValGlyMetLysValAlaLeuGlnValSerMetAsn 300
Db TGTCACAGGCGCTTATCTTAAAGAAAGTTGGCATGAAGCTGCACTCCAGGTCAAGATGAAC 1311


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Qy 301 AepgIyleuSerPheIleSerSerValIleIleThrThrHiCySerIeuHis 320
Db 1312 GATGCCCTCTCTTTATCTCCAGTTCTGTCATCATCACCAACACACTGTAGCTCCAC 1371
Qy 321 LysIleAaSerGlyProThrThrAlaAcyMetGlu 333
Db 1312 AAAATTGCATCAGGCCCAACACACTGCTTCATGGAA 1410

RESULT 8
US-10-038-307-23
/ Sequence 23, Application US/10038307
/ Publication No. US20030134786A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Englin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/038,307
/ CURRENT FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 23
/ LENGTH: 1056
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-038-307-23

Alignment Scores:
Pred. No.: 6,89e-219 Length: 1056
Score: 1718.00 Matches: 332
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.42% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-8 (1-333) x US-10-038-307-23 (1-1056)
Qy 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpIleuSerIeuAlaThr 20
Db 13 ATGGCAGCGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 72
Qy 21 LeuValIleuIleCyAlaGlyGlnGlyValArgArgGluAserGlyProAlaCySerTy 40
Db 73 CTGGGCTCATCTGGCGCGGCGGAGCGGAGCGGAGTGGGAGTCCAGCTGCTAC 132
Qy 41 GlyGlyPheAerPheUtyrPheIleuAerPheSerGlySerValIleuHisIleTrpAn 60
Db 133 GCGGATTTGACCTTACTTCTTCTTTCAGACATCCAGAAAGTGTGCTGCACACCTGGANT 192
Qy 61 GluIleTyTyPheValGluIleuAlaHisIlePheIleSerProGlnIleuArgMet 80
Db 193 GAAATCTATTACTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAAGATG 252
Qy 81 SerPheIleValPheSerThrArgGlyThrThrIleMetIleValIleuArgGlu 100
Db 253 TCCCTTATTGTTTCTCCACCCGAGAAACAACTTAATGAACATGACAGAAACAGAA 312
Qy 101 GluIleAerGlnGlyLeuGlnGluIleuValIleuProGlyValAerThrTyMet 120
Db 313 CAATTCCTGCAAGGCTTGAAAGAACTCCAGAAAGTTCGCGAGGAGAACCTTACATG 372
Qy 121 HisGlnGlyPheGluArgAlaSerGlnGlnIleTyTyGluAserArgGlnGlyTyArg 140
Db 373 CATGAAGATTTGAAAGGCGGAGGAGGAGTATTATTAAGAAACAGCAAGGATACAGG 432
Qy 141 ThrAlaSerValIleIleAlaIleuThrAerGlyGluIleuHisGluAerPheUtyr 160
Db 433 ACAAGCAGGCTCATCTGCTTTCATGCTGATGAGAACTCCATGAAGATCTCTTTTCTAT 492
Qy 161 SerGluArgGluAlaAserAerSerArgAerPheUtyrAlaIleValTyCySerValGlyAl 180

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Db 493 TCAGAGAGGAGGCTAAATAGCTCTGAGATCTGGTGCATATGTTACTGTGTGTGG 552
Qy 181 LysAerPheAerGluThrGlnIleuAlaArgGlyIleAaPserIleAerHisValPhePro 200
Db 553 AAAGATTTCAATGAGACACACTGGCCGAGATGGGACAGTAAGATCATGTGTTCC 612
Qy 201 ValAerAerGlyPheGluAlaIleuGlnGlyIleIleHisSerIleLeuIleYleSerCys 220
Db 613 GTGAATGACGGCTTTCAGGCTCTGCAGGCAATCATCTCAATTTTAAGAAAGTCTGC 672
Qy 221 IleGluIleuAlaIleGluProSerThrIleCyAlaGlyGluSerPheGlnValAl 240
Db 673 ATCGAATTTCTTAGAGGCTGAACCATCCACATATGTCAGAGAGATCATTTCAAGTGTGC 732
Qy 241 ValArgGlyAerGlyPheArgHisAlaArgAerValAerAerValIleuCySerPheIys 260
Db 733 GTGAGAGGAAACGGCTTCCAGATGCCCGCAACGTGACAGAGGTCTCTGCAGCTTCAAG 792
Qy 261 IleAerAerSerValThrIleuAerGluIleuProPheSerValIleuAerThrTyIleu 280
Db 793 ATCAATGACTGGTCACTCAATGAGAAAGCCCTTCTGTGAAAGATATTATTACTG 852
Qy 281 CysProAlaProIleuIleuGlyValGlyMetIleValAlaIleuGlnValSerMetAer 300
Db 853 TGTCCAGGCGCTATCTTAAAGAGTTGGCATGAAGCTGCATCAGTCAAGTCAAGAAC 912
Qy 301 AepgIyleuSerPheIleSerSerValIleIleThrThrHiCySerIeuHis 320
Db 913 GATGCCCTCTCTTTATCTCCAGTTCTGTCATCATCACCAACACACTGTAGCTCCAC 972

RESULT 9
US-10-201-292-23
/ Sequence 23, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Englin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 23
/ LENGTH: 1056
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-23

Alignment Scores:
Pred. No.: 6,89e-219 Length: 1056
Score: 1718.00 Matches: 332
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.42% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-8 (1-333) x US-10-201-292-23 (1-1056)
Qy 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpIleuSerIeuAlaThr 20
Db 13 ATGGCAGCGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 72
Qy 21 LeuValIleuIleCyAlaGlyGlnGlyValArgArgGluAserGlyProAlaCySerTy 40
Db 73 CTGGGCTCATCTGGCGCGGCGGAGCGGAGCGGAGTGGGAGTCCAGCTGCTAC 132

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Qy 41 GlyGlyPheAAspLeuTyrPheIleuAAspSerGlySerValIleuHisIleTPAsn 60
Db 133 GCGGATTTGACCTGACTTCTATTTTGGACAAATCAGAAAGTGTCTGCACACTGGAGT 192
Qy 61 GluIleTyrTyrPheValGluGlnIleuValHisIleValPheIleSerProGlnLeuArgMet 80
Db 193 GAAATCTATTAATTGTTGGAAACAGTTGGCTCACAAAATTCATCAGCCCACTGTGAGATG 252
Qy 81 SerPheIleValPheSerThrArgGlyThrThrIleuMetIleuThrGluAAspArgGlu 100
Db 253 TCTCTTATGTTTCTTCCACCGAGAAACAACTTAATGAAGCTGACAGAAAGACAGAA 312
Qy 101 GlnIleArgGlnGlyLeuGluGlnIleuGlnIleuValIleuProGlyGlyAspThrTyrMet 120
Db 313 CAATCCGTCAGAGGCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACACTG 372
Qy 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAAspArgGlnGlyTyrArg 140
Db 373 CATGAAAGATTTGAAAGGCGCAGTGACAGATTTTATGAAAACAGACAGGATACAG 432
Qy 141 ThrIleSerValIleIleIleIleuThrAspGlyGluMetHisIleuAspLeuPhePheTyr 160
Db 433 ACAGCACCGCTATCATGCTTGTGACTGAGAGAACTCCAGAAAGATCTCTTTTCTAT 492
Qy 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db 493 TCAGAGAGGAGGCGTAATAGCTCGAGATCTGTGGCAATTTGTTTACTGTGTGGTGTG 552
Qy 181 LysAspPheAsnGluThrGlnIleuValAspGlnIleuAAspSerLysAspHisValPhePro 200
Db 553 AAAGATTTCAATGAGACACAGCTGCCCGGATTTGGGACAGTAAGATCATGTGTTTCCC 612
Qy 201 ValAsnAspGlyPheGlnAlaIleuGlnGlyIleIleHisSerIleuValLysSerCys 220
Db 613 GTGAATGACGGCTTTCAGGCTCTGCAAGGCAATCATCTCAATTTTGAAGAGCTCTGC 672
Qy 221 IleGluIleLeuValAlaGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 240
Db 673 ATCGAAATTTCTTAGCGCTGAAACCAATCCACATATGTGAGAGAGTCAATTTCAAGTTGTC 732
Qy 241 ValArgGlyAsnGlyPheArgHisIleAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db 733 GTGAGAGGAAACCGGCTTCGACATGCCCGCAACGTGGACAGGGTCTCTGCAAGCTTCAAG 792
Qy 261 IleAsnAspSerValThrIleuAsnGluLysProPheSerValGluAspThrTyrIleuLeu 280
Db 793 ATCAATGACTGGGTACACTCAATAGAAAGCCCTTTCTGTGGAAGATCAATTTACTG 852
Qy 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaIleuGlnValSerMetAsn 300
Db 853 TGTCCAGGCGCTATCTTAAAGAAAGTTGGCATGAAGGTGCACTCAGCTCAGCATGAGAC 912
Qy 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerLeuHis 320
Db 913 GATGCGCTCTCTTTATCTCCAGTCTGTCTCATCAACACACACACTGTAGCTTCAC 972
Qy 321 LysIleAlaSerGlyProThrThrAlaIleCysMetGlu 333
Db 973 AAAATTGCATGAGGCCCAACACACTGCTTCATGAGAA 1011

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RESULT 10 US-10-038-307-21

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; Sequence 21, Application US/10038307
; Publication NO. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038.307

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; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PASTESEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-21

Alignment Scores:
Pred. No.: 2,71e-218 Length: 1047
Score: 1713.50 Matches: 333
Percent Similarity: 97.37% Conservative: 0
Best Local Similarity: 97.37% Mismatches: 0
Query Match: 99.16% Indels: 9
DB: 15 Gaps: 1

US-09-970-076-8 (1-333) x US-10-038-307-21 (1-1047)
Qy 1 MetAlaThrAlaGluArgAlaIleuGlyIleGlyPheGlnIleuSerLeuAlaThr 20
Db 13 ATGCGCACGCGGAGCGGAGAGCCCTCGCATCGGCTTCCAGTGGCTCTCTTGGCCACT 72
Qy 21 LeuValIleuIleCysAlaGlyGlnGlyIleArgArgGluAspGlyIlePro----- 37
Db 73 CTGGTCTCATCTGCGCGCGGCAAGGGGACGCGAGGAGATGGGGGTCCAAATGATTAAC 132
Qy 38 -----AlaCysTyrGlyGlyPheAspLeuTyrPheIleuAspLys 51
Db 133 AAGGATACATGATGACAAAGGCTGTCTACGGGATTTACCTGTGATCTTCAATTTTGGACAA 192
Qy 52 SerGlySerValIleuHisIleTPAsnGluIleTyrTyrPheValGluGlnLeuValHis 71
Db 193 TCAGGAAGTGTGCGCACCACTGGAATGAATCATTAATTTGGAAACAGTTGGCTCAC 252
Qy 72 LysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThr 91
Db 253 AAATTCATGACGCCACACAGTTGAGATGTCTTTATTTCTTCCACCCGAGAAACACC 312
Qy 92 LeuMetLysLeuThrArgIleuAspArgGluGlnIleAspGlnIleuGlnLys 111
Db 313 TTAATGAATCTGACAGAAAGACAGAAACAAATCCGTCAAGGCTCAAGAACTCCAGAA 372
Qy 112 ValIleuProGlyGlyAspThrTyrMetHisIleGlyPheGluArgAlaSerGluGlnIle 131
Db 373 GTTCTGCAAGAGGAGACACTTACATGATGAAGATTTGAAAGGCGCAATGACAGAT 432
Qy 132 TyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGly 151
Db 433 TATTATGAAACAGACAAAGGGTACAGAGACAGCCGCTCATCATTCCTTGAATGATGA 492
Qy 152 GluIleuHisIleGluAspLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeu 171
Db 493 GAACTCATGAAGATCTCTTTTCTATTATTCAGAGAGGAGGCTTAATAGCTTCGAGACT 552
Qy 172 GlyAlaIleValTyrCysValGlyValIleAspPheAsnGluThrGlnLeuAlaArgIle 191
Db 553 GGTGCATATTGTTTACTGTGTGTGTGTAAGATTTCAATGAGACACAGCTGGCCGAGATT 612
Qy 192 AlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaIleuGlnGlyIle 211
Db 613 GCGGACAGTAAGATCATGTGTTCCCGTAATGACGCGCTTTCAGGCTTCGACAGGATC 672
Qy 212 IleHisSerIleLeuLysLysSerCysIleGlnIleuValAlaGluProSerThrIle 231
Db 673 ATCCACTCAATTTTGAAGAAAGCTCTGCATGAAATTTAGAGGTGAACCATTCACCACTA 732
Qy 232 CysAlaGlyLysSerPheGlnValValIleArgGlyAsnGlyPheArgHisIleAlaArgAsn 251
Db 733 TGTGCAAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTTCCAGATGCCGCGCAC 792
Qy 252 ValAspArgValLeuCysSerPheLysIleAsnAspSerValThrIleuAsnGluLysPro 271

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Best Local Similarity:	97.268	Mismatches:	2
Query Match:	95.528	Indels:	5
DB:	15	Gaps:	1

RESULT 13
US-10-201-292-17
; Sequence 17, Application US/10201292
; Publication No. US2003014193A1

OY	1	MetLethrAlaGluArgAlaAlaGly11LeuYpHeGIntPrLseLseLethr	20
Db	13	ATGGCCACGGGGAGCGGAGCCCTCGGAGATCGGCTTCAGTGGCTCTTTGGACACT	72
OY	21	LeuValLeu1LeCysAlaG1yG1nG1yG1ArgArgGluAspG1yG1ProAlaCysTyr	40
Db	73	CTGGTGCTCATCTGGCGCGGCGGCAAGGGGAGCCAGGAGAGATGGGGGCTTCAGCTGTAC	122
OY	41	G1yG1PheAspLeuTyrPhe11LeuAspLysSerG1ySerValLeu1nH1SerTrpAsn	60
Db	133	GGCGGATTTGACCTGTAATTCATTTGGCAAAATCAGAAAGTGTCGTSCAACCTGGAAAT	192
OY	61	Glu1Le1yTyrPheValGluGlnLeuAlaH1b1yPhe11LeSerProGlnLeuAlaMet	80
Db	193	GAATCTAATTAATTTGGGAAACGTTGGCTGCACAAATTCATCAGCCACAGTTGAGATG	252

```

; APPLICANT: James B. ROTTMAN
; APPLICANT: Thereasa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-553-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-17

```

Oy	8	SerPheIleValPheSerThrArgGlyThrThrIleuMetLeuIleuThcGluAspArgGlu	100
Db	253	TCCTTATTGTTTTCTCCACCAGGAACAACCTTAATGAACATGACGAAGAACAAGAA	312
Oy	101	GlnIleArgGlnGlyLeuGlnGluLeuGlnIleValLeuProGlyValAspThrTyrMet	120
Db	313	CAAAATCGGTAAAGGCGCTAGAAAGAACTCCAGAAAGTTCTCCAGAGAGAGAACATTACATG	372
Oy	121	HisGlnGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg	140
Db	373	CATAAAGATTGAAAGGCGCAGTAGAGCAAGATTATTATGAAACAGACAAAGGTTAACAGG	432
Oy	141	ThrIleAspValIleIleIleAlaLeuThrArgGlyGluIleHisGluAspLeuPhePheTyr	160
Db	433	ACAGCCAGCGTCATCATGTCTTGAGCTAGTAGAGAACTCCAGAAAGATCTCTTTTCTAT	492
Oy	161	SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal	180
Db	493	TCAGAGAGGAGGCTAAATAGTGTCCAGATCTTGCGCAATGTTTACTGTGTGGGTGG	553
Oy	181	LysAspPheAsnGluThrGlnIleuAlaArgIleAlaAspSerLysAspHisValPhePro	200
Db	553	AAAGATTTCATGAGACACACAGCTGGCCGGATTGGCGACAGTAAGATCATGTGTTCCC	612
Oy	201	ValAlaAsnArgGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys	220
Db	613	GTCGATACACGGCTTTCAAGGCTTCGACAGGACATCATCCACTCAATTGTAAAGATGCTGTC	672
Oy	221	IleGlnIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal	240
Db	673	ATCGAAATTTTAGCAGCTGACCACTCCACCAATATGTGCAGAGAACTCATTCGAAAGTTGTC	732
Oy	241	ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys	260
Db	733	GTGAGAGGAACGGCTTCCGACATGCCCGCAACGTGACAGGCTCTCTGCAGCTTCAG	792
Oy	261	IleAsnAspSerValThrIleuAsnGlyLysProPheSerValGluAspThrTyrLeuLeu	280
Db	793	ATCATATACCTCGGTACACACTCAATGGAAGCCCTTTCTGTGGAGATACATTATTCTCG	852
Oy	281	CysProAlaProIleLeuLysGlyValGlyMetLysAlaAlaLeuGlnValSerMetAsn	300
Db	853	TGTCACCGGCTATTCTTAAGAAGATTGCACGAAAGCTGCACTCCAGTAGCATATAC	912
Oy	301	AspGlyLeuSerPheIleSerSerSerValIleIleIleThrThrHisCysSerLeuHis	320
Db	913	GATGGCTCTCTTTATCTCCAACTTGTGCATCATCACCAACAACAATGTTCT-----	966
Oy	321	LysIleAlaSerGlyProThrThrAla	329
Db	967	-----GACGGTCCCAAAATCTTCT	984

Alignment Scores:			
Pred. No.:	1.56e-209	Length:	1674
Score:	1650.50	Matches:	320
Percent Similarity:	97.87%	Conservative:	2
Best Local Similarity:	97.26%	Mismatches:	2
Query Match:	95.52%	Indels:	5
DB:	15	Gaps:	1
US-09-970-076-8 (1-333) x US-10-201-292-17 (1-1674)			
QY	1	MetaLThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr	20
DB	13	ATGGCCAGCGGGAGCGGAGAGCCCTCGCATCGGCTTCAGTGGCTCTCTTGGCCACT	72
QY	21	LeuValLeuIleCybAlaGlyGlnGlyValArgArgGluAspGlyGlyProAlaCysTrp	40
DB	73	CTGGTGCTCATCTCGCCGGCAAGGGGAGACGACGAGAGATGGGGGTCCAGCCTGTAC	132
QY	41	GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuIleHisTrpAsn	60
DB	133	GCGGATTTGACCTGTACTTCATTTTGGACAAACAGAAAGTGTGTGCACCACTGAAAT	192
QY	61	GluIleTrpTrpPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet	80
DB	193	GAATCTATTACTTTGTGGAACTGTGGCTCACAAATTCATCAGCCACAGTTGAGAAATG	252
QY	81	SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu	100
DB	253	TCTTTTATTGTTTTCTCCACCAGGAACAACCTTATGAAACTGACAGAAAGACAGAA	312
QY	101	GlnIleArgGlnGlyLeuGluGlnLeuGlnLysValLeuProGlyGlyAspThrTrpMet	120
DB	313	CAATCCGTCAGGCGCTCAGAGAACTCCAGAAATTTCTGCCAGAGAGAGACACTTACATG	372
QY	121	HisGluGlyPheGluArgAlaSerGluGlnIleTrpTrpGluAsnArgGlnTrpArg	140
DB	373	CATGAGGATTTGAAAGGCGCATGACACAGATTTATTATGAAACAACAAGGGTACAGG	432
QY	141	ThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGluAspLeuPhePheTrp	160
DB	433	ACAGCGAGCGTCATCATTTGCTTGCATGATGAGAACTCCATGAAAGATCTCTTTTCTAT	492
QY	161	SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTrpCysValGlyVal	180
DB	493	TCAAGAGGGGAGCTAATAGGTCTCGAGATCTTGTCCAATTGTTTACTGTGTGCTGTG	552
QY	181	LysAspPheAsnGluTrpGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro	200
DB	553	AAAGATTTCAATGACACACAGCTGGCCCGGATTTGCCGACGTAAGATCATGTGTTTCC	612
QY	201	ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys	220

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Db      613 GTGATGACGGCTTCAAGCTCTGCAGACATCATCTCAATTTTGAAGAATCCTGC 672
Qy      221 IIEGUILLEUAlAAlaGluProSerThrIIEySaIaGlyGluSerPheGlnValaI 240
Db      673 ATCGAATTTCTAGCAGCTGAGACATCCATCATATGTGCGAGAGATCTCAATTTGCTGC 732
Qy      241 VALAARGGIAANGIYPhehArgHISAlaArgenValaAPaArgValaLeuCySerPheIys 260
Db      733 GTGAAGAGAAACGGCTTCGACATGCTCCGACACGTGACAGGGCTCTCTGCAGCTTCAAG 792
Qy      261 IIEaenAPSerValThrleuAnGluIysProPheSerValaGluAPThrTYrleuLeu 280
Db      793 ATCAATGACTCGCTCACTCACTCAATGAGAACCCCTTTCTGTGAGAAATATTATTACTG 852
Qy      281 CyPProAlaProIIEleuIysGluValaGlyMeIySaIaAlaLeuGlnValSerMetAsn 300
Db      853 TGTCCAGCGCTATCTTAAAGAGAGTGGCATGAAGCTGCACTCCAGGTCCAGATGAAC 912
Qy      301 AArgGlyLeuSerPheIIEserSerValIIEIIEThrThrThiScySerLeuHis 320
Db      913 GATGACCTCTCTTTATCTCCAGTTCTGTGCATCATCATCACACACACTGTTCT----- 966
Qy      321 LySIEAlaSerGIYProThrThAla 329
Db      967 -----GACGCTCCAAATCTTCT 984

RESULT 14
US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; FILE REFERENCE: OTHER BIOLOGICAL STATES
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:
Pred. No.: 1,966-209 Length: 1454
Score: 1649.00 Matches: 318
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.43% Indels: 0
DB: 16 Gaps: 0

US-09-970-076-8 (1-333) x US-10-133-937-58 (1-1454)
Qy      1 MetAlaThrAlaGluArgArgAlaLeuGlyIIEGlyPheGlnThrLeuSerLeuAlaThr 20
Db      144 ATGGCCACGGCGGAGAGAGAGCCCTCGGCATCGGCTTCATGCTCTCTTTGGCCACT 203
Qy      21 LeuValLeuIIECyenIaGlyGlnGlyIATArgATGGLuAPArgIYGIYProAlaCySyr 40
Db      204 CTGGGTGCTATCTGGCGCGGAGGAGGCCAGCCAGGAGAGATGGGGGTCTCACTGCTAC 263
Qy      41 GIYGIYPheAPLeuTYrPheIIEleuAPlySerGIYSerValLeuHISHTPAsn 60
Db      264 GCGCGATTTCACCTGATCTTCAATTTTGGCAAAATCAGAAAGTGTCTGCACCACTGGAAT 323
Qy      61 GUILIEYTYrPheValGluGlnLeuAlaHISlybPheIIEserProGlnLeuArgMet 80

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Db      324 GAATCTATTACTTTGTGGAACAAGTGGCTCACAATTCATCAGCCACAGTTGAATG 383
Qy      81 SerPheIIEValPheSerThrArgGIYThrThrleuMetIySleuThrGluAPArgGlu 100
Db      384 TCTTTATTTGTTTCTCCACCCGAGGAACAACCTTAATGAAGATGACAGAAACAGAA 443
Qy      101 GlnIIEArgGlnGlyLeuGlnGluLeuGlnIySValIIEuProGlyGIYAspThrTYrMet 120
Db      444 CAATTCCTCAAGGCTTGAAGAACTCGAAGAGTTCTGCGAGGAGAGACATTACATG 503
Qy      121 HIEGULIYPheGluArgAlaSerGIUglnIIEYTYrGIYAsnArgGlnIYTYrArg 140
Db      504 CATGAAGATTGAAAGGCCAGTGAAGCATTTATTATGAAGAACAGCAAGAGGTACAG 563
Qy      141 ThrAlaSerValIIEIIEAlaLeuThrAPGlyGluLeuHISGluAPLeuPhePheTYr 160
Db      564 ACAGCCAGCGTCATCATCTTGTGATGATGAGAACTCCATGAAGATCTCTTTTCTAT 623
Qy      161 SerGIUArgGluAlaAsnArgSerArgAPLeuGlyAlaIIEValTYrCyValGIYVal 180
Db      624 TCAGAGAGGAGGCTTAATAGGTCCTGAGATCTGTGCAATTTGTTACTGTGTGTGTG 683
Qy      181 LySAPPheAnGluTYrGlnLeuAlaArgIIEAlaAPSerLySAPHISValPhePro 200
Db      684 AAAGTTTCATGACACACACACTGCGCCGAGTTGGGACATGAAGATCATGTGTTTCC 743
Qy      201 ValAsnAPGIYPheGlnAlaLeuGlnGlyIIEIIEHISerIIEleuIySleuCyS 220
Db      744 GTGAATGACGGCTTCAAGCTCTGCAAGCATCATCTCAATTTTGAAGAAGCTCTGC 803
Qy      221 IIEGUILLEUAlAAlaGluProSerThrIIEySaIaGlyGluSerPheGlnValaI 240
Db      804 ATCGAATTTCTAGCAGCTGGAACCATCCCATATGTGAGAGAGTCAATTCAGATTTC 863
Qy      241 VALAARGGIAANGIYPheArgHISAlaArgenValaAPaArgValaLeuCySerPheIys 260
Db      864 GTGAGAGAAACGGCTTCGACATGCTCCGACACGTGACAGGGTCTCTGCAGCTTCAAG 923
Qy      261 IIEaenAPSerValThrleuAnGluIysProPheSerValaGluAPThrTYrleuLeu 280
Db      924 ATCAATGACTCGCTCACTCAATGAGAACCCCTTTCTGTGAGAAACATTAATTACTG 983
Qy      281 CyPProAlaProIIEleuIysGluValaGlyMeIySaIaAlaLeuGlnValSerMetAsn 300
Db      984 TGTCCAGCGCTATCTTAAAGAGTGGCATGAAGCTGCATCCAGTCAAGCATYGAAC 1043
Qy      301 AArgGlyLeuSerPheIIEserSerValIIEIIEThrThrThiScySer 318
Db      1044 GATGACCTCTCTTTATCTCCAGTTCTGTGCATCATCATCACACACACTGTTCT 1097

RESULT 15
US-10-159-563-58
; Sequence 58, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens

```

US-10-159-563-58

Alignment Scores:

Pred. No.:	1,966-209	Length:	1454
Score:	1649.00	Matches:	318
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.43%	Indels:	0
DB:	16	Gaps:	0

US-09-970-076-8 (1-333) x US-10-159-563-58 (1-1454)

QY	1	MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr	20
DB	144	ATGGCCACGGCGGAGAGAGACCTCGGCAATCGGCTTCAGTGGCTCTCTTTGGCCACT	203
QY	21	LeuValIleuIleCysAlaGlyGlnGlyIleArgAlaArgGlyIleProAlaCysTyr	40
DB	204	CTGGTCTCATCTGGCGCGGAGGAGACGACAGGAGAGTGGGGTCCAGCCCTGCTAC	263
QY	41	GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn	60
DB	264	GGCGGATTTGACCTTACTTCTTTCATTCAGAAATCAGAAAGTGTCTGCACCACTGGAAAT	323
QY	61	GluIleTyrTyrPheValGluGlnLeuAlaHisIlyPheIleSerProGlnLeuArgMet	80
DB	324	GAAATCTATTACTTGTGGACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATG	383
QY	81	SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu	100
DB	384	TCTTTATTTGTTTCTCCACCGAGGAAACAACTTAATGAACCTGACAGAAAGACAGAA	443
QY	101	GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet	120
DB	444	CAAAATCCGTCAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG	503
QY	121	HisGlyIlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg	140
DB	504	CATGAAGATTGAAAGGCGCCAGTAGCAGATTATTATGAAAAACAGCAAGGGTACAG	563
QY	141	ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr	160
DB	564	ACAGCCAGCGTCATATGCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT	623
QY	161	SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal	180
DB	624	TCAAGAGGAGGAGCTAATAGCTTCGAGATCTTGGTGCATTTGTTACTGTGTGTGTG	683
QY	181	LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro	200
DB	684	AAAGATTTCATGAGACACAGCTGGCCCGGATTCGGAACATGATCATGTGTTTCCC	743
QY	201	ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys	220
DB	744	GTAATGACGGCTTCAGGCTCTGCAAGGACATCCACTCAATTTGAAAGAGCTCTGC	803
QY	221	IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal	240
DB	804	ATCGAAATTTTCAGACGCTGAAACATCCACATATGTGCAGAGAGTCAATTCAGATTGTC	863
QY	241	ValAlaArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys	260
DB	864	GTAAGAGGAAAGGCTTCGACATCCGCAACGTGACAGGGTCTCTGCAGCTTCAAG	923
QY	261	IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu	280
DB	924	ATCATATGACTCGGTACACTCATATGAGAGCCCTTTCTGTGAGAGACATTAATTACTG	983
QY	281	CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn	300
DB	984	TGTCCAGCGCTCATTTTAAAGAAAGTTGGCATGAAAGCTGCACCTCAGGTCAAGCATGAA	1043
QY	301	AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSer	318

DB

1044 GATGGCTCTCTTTATCTCCAGTTCTGTCAATCATCACACACACTGTTCT 1097

Search completed: June 22, 2004, 08:11:28
Job time : 508.02 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:39:51 / Search time 12.5745 Seconds

(without alignments)
1367.166 Million cell updates/sec

Title: US-09-970-076-8

Perfect score: 1728
Sequence: 1 MATERRALGFGFWLSLAT.....TTHCSIMKIASGPTTACME 333

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	9.6	1155	1 US-08-286-889-46	Sequence 46, Appl
2	166	9.6	1155	1 US-08-485-618-46	Sequence 46, Appl
3	166	9.6	1155	1 US-08-362-652-46	Sequence 46, Appl
4	166	9.6	1155	2 US-08-605-672-46	Sequence 46, Appl
5	166	9.6	1155	2 US-08-482-293A-46	Sequence 46, Appl
6	166	9.6	1155	2 US-08-943-363-46	Sequence 46, Appl
7	166	9.6	1155	3 US-09-193-043-46	Sequence 46, Appl
8	166	9.6	1155	4 US-09-688-307A-46	Sequence 46, Appl
9	166	9.6	1155	4 US-09-350-259-46	Sequence 46, Appl
10	166	9.6	1161	1 US-08-485-618-53	Sequence 53, Appl
11	166	9.6	1161	1 US-08-362-652-53	Sequence 53, Appl
12	166	9.6	1161	2 US-08-605-672-53	Sequence 53, Appl
13	166	9.6	1161	2 US-08-482-293A-53	Sequence 53, Appl
14	166	9.6	1161	2 US-08-943-363-53	Sequence 53, Appl
15	166	9.6	1161	3 US-09-193-043-53	Sequence 53, Appl
16	166	9.6	1161	4 US-09-688-307A-53	Sequence 53, Appl
17	166	9.6	1161	4 US-09-350-259-53	Sequence 53, Appl
18	159.5	9.2	1151	1 US-08-286-889-37	Sequence 37, Appl
19	159.5	9.2	1151	1 US-08-485-618-37	Sequence 37, Appl
20	159.5	9.2	1151	1 US-08-362-652-37	Sequence 37, Appl
21	159.5	9.2	1151	2 US-08-605-672-37	Sequence 37, Appl
22	159.5	9.2	1151	2 US-08-482-293A-37	Sequence 37, Appl
23	159.5	9.2	1151	2 US-08-943-363-37	Sequence 37, Appl
24	159.5	9.2	1151	3 US-09-193-043-37	Sequence 37, Appl
25	159.5	9.2	1151	4 US-09-688-307A-37	Sequence 37, Appl
26	159.5	9.2	1151	4 US-09-350-259-37	Sequence 37, Appl
27	159.5	9.2	1161	1 US-08-173-497-2	Sequence 2, Appl

28	159.5	9.2	1161	1 US-08-286-889-2	Sequence 2, Appl
29	159.5	9.2	1161	1 US-08-485-618-2	Sequence 2, Appl
30	159.5	9.2	1161	1 US-08-362-652-2	Sequence 2, Appl
31	159.5	9.2	1161	1 US-08-605-672-2	Sequence 2, Appl
32	159.5	9.2	1161	1 US-08-482-293A-2	Sequence 2, Appl
33	159.5	9.2	1161	1 US-08-943-363-2	Sequence 2, Appl
34	159.5	9.2	1161	2 US-08-605-672-2	Sequence 2, Appl
35	159.5	9.2	1161	2 US-08-482-293A-2	Sequence 2, Appl
36	159.5	9.2	1161	2 US-08-943-363-2	Sequence 2, Appl
37	159.5	9.2	1161	2 US-08-605-672-2	Sequence 2, Appl
38	159.5	9.2	1161	2 US-08-482-293A-2	Sequence 2, Appl
39	159.5	9.2	1161	2 US-08-943-363-2	Sequence 2, Appl
40	159.5	9.2	1161	2 US-08-605-672-2	Sequence 2, Appl
41	159.5	9.2	1161	2 US-08-482-293A-2	Sequence 2, Appl
42	159.5	9.2	1161	2 US-08-943-363-2	Sequence 2, Appl
43	159.5	9.2	1161	2 US-08-605-672-2	Sequence 2, Appl
44	159.5	9.2	1161	3 US-09-193-043-2	Sequence 2, Appl
45	159.5	9.2	1161	3 US-09-688-307A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-286-889-46
Sequence 46, Application US/08286889
Patent No. 5470953
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 233 South Wacker Drive, 6300 Seair Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286, 889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-46
Query Match 9.6%, Score 166, DB 1, Length 1155;
Best Local Similarity 28.2%, Pred. No. 3.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
37 PACYG-GDLYFIIDKSGSV-LHMHNEIYYVEQIAHFKFISPOLRMSFVSTGTTLMK 94

Db 144 PECGQEMDIAPFLIDSGSIDSDFTQMKDFVKALMQLASTSTSPSIMOYSNLIKTHPT 203
Qy 95 LTEDR-----EQIROGLEBLQKVLPGDITYMHGFERASBOIYYENRGYRTA-SVITAL 148
Db 204 FTEFKSSLSPOSLVAIVQLO-----GLTYTASGIQKVVLELPHSKNGARKSAKKILIVI 258
Qy 149 TDGELHEDLFFYSE--REANRSRLGAIIVYCVGKD-FNE-TOLARI-----ADSKDHVF 199
Db 259 TDGQKFRDPLEYRHVYIPEAEKA---GIIRYALGVGDAREPTALQELNTIGSAPSQDHVF 315
Qy 200 PVDNFOALOGIITHSLKSCIEILAEPSITCAGESFOVVRNGGFRHARNVD 253
Db 316 KVGK-FVALRSIQROIQOEK----IFAIGTESRSSSSFQHEMSQGFSSALSMD 364

RESULT 2

US-08-485-618-46
; Sequence 46, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Seear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/485,618
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-618-46

Query Match 9.6%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 3,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
Qy 37 PACYG-GPDLYFIILKSGSV-LHHNEIYFVEQLAHKFIISPOLRMSFIVSTGTITLMK 94
Db 144 PECGQEMDIAPFLIDSGSIDSDFTQMKDFVKALMQLASTSTSPSIMOYSNLIKTHPT 203

Qy 95 LTEDR-----EQIROGLEBLQKVLPGDITYMHGFERASBOIYYENRGYRTA-SVITAL 148
Db 204 FTEFKSSLSPOSLVAIVQLO-----GLTYTASGIQKVVLELPHSKNGARKSAKKILIVI 258
Qy 149 TDGELHEDLFFYSE--REANRSRLGAIIVYCVGKD-FNE-TOLARI-----ADSKDHVF 199
Db 259 TDGQKFRDPLEYRHVYIPEAEKA---GIIRYALGVGDAREPTALQELNTIGSAPSQDHVF 315
Qy 200 PVDNFOALOGIITHSLKSCIEILAEPSITCAGESFOVVRNGGFRHARNVD 253
Db 316 KVGK-FVALRSIQROIQOEK----IFAIGTESRSSSSFQHEMSQGFSSALSMD 364

RESULT 3

US-08-362-652-46
; Sequence 46, Application US/08362652
; Patent No. 576850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 576850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Seear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/362,652
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-362-652-46

Query Match 9.6%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 3,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
Qy 37 PACYG-GPDLYFIILKSGSV-LHHNEIYFVEQLAHKFIISPOLRMSFIVSTGTITLMK 94
Db 144 PECGQEMDIAPFLIDSGSIDSDFTQMKDFVKALMQLASTSTSPSIMOYSNLIKTHPT 203
Qy 95 LTEDR-----EQIROGLEBLQKVLPGDITYMHGFERASBOIYYENRGYRTA-SVITAL 148
Db 204 FTEFKSSLSPOSLVAIVQLO-----GLTYTASGIQKVVLELPHSKNGARKSAKKILIVI 258
Qy 149 TDGELHEDLFFYSE--REANRSRLGAIIVYCVGKD-FNE-TOLARI-----ADSKDHVF 199

Db 259 TDGQFRPDLRYHVIPEAKA---GIRYAGVGDAREPFAALQELMTIGSAPSQDHVF 315
Qy 200 PVNDGFOALQGIHSLKSCIEIILAAEPSTTCAGESQVAVVNGGFRHARNVD 253
Db 316 KVG-N-FVALRSIQROIQEK---IPALEGTESRSSSSSFQHEMSQGFSSALSMD 364

RESULT 4

US-08-605-672-46
Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESS: Marshhall, O'Toole, Gerstein, Murray & Borum
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-46

Query Match 9.6%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 3.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
Qy 37 PACYV-GPDLYFILDKSGSV-LHWNELIYFVEQLAHKFIISPOLMSFIVSTRTGLMK 94
Db 144 PECQEQENDIAFLIDSGSISDQSDFTQMKDFVKALMGQLASTSTFSIMQYSNLIKHTHT 203
Qy 95 LTEDR-----EQIRQGLELQKVLPGSDTYMHGEFERASEQIYYENROGYTA-SVIAL 148
Db 204 FTEFKSSISPSQSLVDALVQLQ-----GLTYASGIQKVKELFHSKNGARKSAKKILIVI 258
Qy 149 TDGELHEDLFYYSR--REANRSRDIGAIYVCVGD-FNE-TQLARI-----ADSKDHVF 199
Db 259 TDGQFRPDLRYHVIPEAKA---GIRYAGVGDAREPFAALQELMTIGSAPSQDHVF 315

Qy 200 PVNDGFOALQGIHSLKSCIEIILAAEPSTTCAGESQVAVVNGGFRHARNVD 253
Db 316 KVG-N-FVALRSIQROIQEK---IPALEGTESRSSSSSFQHEMSQGFSSALSMD 364

RESULT 5

US-08-482-293A-46
Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESS: Marshhall, O'Toole, Gerstein, Murray & Borum
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-46

Query Match 9.6%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 3.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
Qy 37 PACYV-GPDLYFILDKSGSV-LHWNELIYFVEQLAHKFIISPOLMSFIVSTRTGLMK 94
Db 144 PECQEQENDIAFLIDSGSISDQSDFTQMKDFVKALMGQLASTSTFSIMQYSNLIKHTHT 203
Qy 95 LTEDR-----EQIRQGLELQKVLPGSDTYMHGEFERASEQIYYENROGYTA-SVIAL 148
Db 204 FTEFKSSISPSQSLVDALVQLQ-----GLTYASGIQKVKELFHSKNGARKSAKKILIVI 258
Qy 149 TDGELHEDLFYYSR--REANRSRDIGAIYVCVGD-FNE-TQLARI-----ADSKDHVF 199
Db 259 TDGQFRPDLRYHVIPEAKA---GIRYAGVGDAREPFAALQELMTIGSAPSQDHVF 315
Qy 200 PVNDGFOALQGIHSLKSCIEIILAAEPSTTCAGESQVAVVNGGFRHARNVD 253

Db 316 KVGK-FVALRSIQRIQIERK-----IPALIGTSSRSSSSFOHEMGOEGFSSALSMD 364

RESULT 6
US-08-943-363-46
Sequence 46, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seat Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: William Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-46

Query Match 9.6%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 3,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
Db 37 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSFIYSTGTITLMK 94
144 PECPGQEMDIAFLIDGSGSIDQSDPTQKDFVAKLMGQLASTSTSFSLMOTSNIUKTHFT 203
95 LTEDR-----EQIROGIELELOKVLPGGDTYMHGFEFASQIYYENROGYRTA-SVIAL 148
204 FTERFKSLSPQSLVDIAVQLO-----GLTYTASGIQKVVELFHSKNGAKRSACKILIVI 258
149 TDGELHEDLFFYSE--REANRSRDLAGIYVCVGYKD-FNE-TOLARI-----ADSKOHVF 199
259 TDGQKFRDPLFERYHVIPEAKA---GIIRYALIGVDAREPTALQELNTTIGSAPSQDHVF 315
200 PVNDGFOLGIIHSLKSCIEILAAPSTICAGSEFOYVVRNGRFRHARNVD 253
316 KVGK-FVALRSIQRIQIERK-----IPALIGTSSRSSSSFOHEMGOEGFSSALSMD 364

RESULT 7
US-09-193-043-46
Sequence 46, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-193-043-46

Query Match 9.6%; Score 166; DB 3; Length 1155;
Best Local Similarity 28.2%; Pred. No. 3,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
Db 37 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSFIYSTGTITLMK 94
144 PECPGQEMDIAFLIDGSGSIDQSDPTQKDFVAKLMGQLASTSTSFSLMOTSNIUKTHFT 203
95 LTEDR-----EQIROGIELELOKVLPGGDTYMHGFEFASQIYYENROGYRTA-SVIAL 148
204 FTERFKSLSPQSLVDIAVQLO-----GLTYTASGIQKVVELFHSKNGAKRSACKILIVI 258
149 TDGELHEDLFFYSE--REANRSRDLAGIYVCVGYKD-FNE-TOLARI-----ADSKOHVF 199
259 TDGQKFRDPLFERYHVIPEAKA---GIIRYALIGVDAREPTALQELNTTIGSAPSQDHVF 315
200 PVNDGFOLGIIHSLKSCIEILAAPSTICAGSEFOYVVRNGRFRHARNVD 253
316 KVGK-FVALRSIQRIQIERK-----IPALIGTSSRSSSSFOHEMGOEGFSSALSMD 364

RESULT 8
US-09-688-307A-46
Sequence 46, Application US/09688307A
Patent No. 6432404
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR FILING DATE: 1997-10-03

NUMBER OF SEQ ID NOS: 114
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 46
 LENGTH: 1155
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-688-307A-46

Query Match 9.6%; Score 166; DB 4; Length 1155;
 Best Local Similarity 28.2%; Pred. No. 3.4e-09;
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACVY-GRDLYFILDKSGSV-LHHNNEIYFVEQLAHKEISPOLMSPFVSTRTGLMK 94
 DB 144 PEPQOEMDIAPLIDSGSIDSDPTOMKDFKALMGQLASTSTSPSLMOYSNLIKTHFT 203
 QY 95 LTEDR-----EQIROGLELQVLPBGDTYMHGFERASEQIYENROGYRTA-SVIAL 148
 DB 204 FTEFSSLSPOSTLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILLYI 258
 QY 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVKD-FNE-TOLARI-----ADSKDHYF 199
 DB 259 TDGQKFRPDLBYRHVYIPEAEKA---GIIRYAIQVGDAREPPTALQELMTIGSAPQDHYF 315
 QY 200 PVDGFOALQGIHSLKSCIEILAEPSITCAGESFOVYVVRNGFPHARVD 253
 DB 316 KGN-FVALRSIQROIQEK---IFAIEGTSSRSSSFQHEMSQGFSSALSM 364

RESULT 9

US-09-350-259-46
 Sequence 46, Application US/09350259
 Patent No. 6620915

GENERAL INFORMATION:
 APPLICANT: Gallatin, Michael W.
 APPLICANT: Van der Vieren, Monica
 TITLE OF INVENTION: No. 6620915el Human 2
 FILE REFERENCE: 27866/35004
 CURRENT APPLICATION NUMBER: US/09/350,259
 FILING DATE: 1999-07-08
 EARLIER APPLICATION NUMBER: 09/193,043
 EARLIER FILING DATE: 1998-11-16
 EARLIER APPLICATION NUMBER: 08/113,497
 EARLIER FILING DATE: 1993-12-23
 EARLIER APPLICATION NUMBER: 08/286,889
 EARLIER FILING DATE: 1994-08-05
 EARLIER APPLICATION NUMBER: 08/362,652
 EARLIER FILING DATE: 1994-12-21
 EARLIER APPLICATION NUMBER: 08/943,363
 EARLIER FILING DATE: 1997-10-03
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 46
 LENGTH: 1155
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-350-259-46

Query Match 9.6%; Score 166; DB 4; Length 1155;
 Best Local Similarity 28.2%; Pred. No. 3.4e-09;
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACVY-GRDLYFILDKSGSV-LHHNNEIYFVEQLAHKEISPOLMSPFVSTRTGLMK 94
 DB 144 PEPQOEMDIAPLIDSGSIDSDPTOMKDFKALMGQLASTSTSPSLMOYSNLIKTHFT 203
 QY 95 LTEDR-----EQIROGLELQVLPBGDTYMHGFERASEQIYENROGYRTA-SVIAL 148
 DB 204 FTEFSSLSPOSTLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILLYI 258
 QY 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVKD-FNE-TOLARI-----ADSKDHYF 199
 DB 259 TDGQKFRPDLBYRHVYIPEAEKA---GIIRYAIQVGDAREPPTALQELMTIGSAPQDHYF 315

QY 200 PVDGFOALQGIHSLKSCIEILAEPSITCAGESFOVYVVRNGFPHARVD 253
 DB 316 KGN-FVALRSIQROIQEK---IFAIEGTSSRSSSFQHEMSQGFSSALSM 364

RESULT 10

US-08-485-618-53
 Sequence 53, Application US/08485618
 Patent No. 5728533

GENERAL INFORMATION:
 APPLICANT: Gallatin, W. Michael
 APPLICANT: Van der Vieren, Monica
 TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
 NUMBER OF SEQUENCES: 103
 CORRESPONDENCE ADDRESSES:
 ADDRESS: Marshall, O'Toole, Gerstein, Murray & Bornun
 STREET: 233 South Wacker Drive, 6300 Sear Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,618
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/173,497
 FILING DATE: 23-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,889
 FILING DATE: 5-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/362,652
 FILING DATE: 21-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams Jr., Joseph A.
 REGISTRATION NUMBER: 38,659
 TELEPHONE/DOCKET NUMBER: 27866/32797
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1161 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-485-618-53

Query Match

9.6%; Score 166; DB 1; Length 1161;
 Best Local Similarity 28.2%; Pred. No. 3.4e-09;
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACVY-GRDLYFILDKSGSV-LHHNNEIYFVEQLAHKEISPOLMSPFVSTRTGLMK 94
 DB 144 PEPQOEMDIAPLIDSGSIDSDPTOMKDFKALMGQLASTSTSPSLMOYSNLIKTHFT 203
 QY 95 LTEDR-----EQIROGLELQVLPBGDTYMHGFERASEQIYENROGYRTA-SVIAL 148
 DB 204 FTEFSSLSPOSTLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILLYI 258
 QY 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVKD-FNE-TOLARI-----ADSKDHYF 199
 DB 259 TDGQKFRPDLBYRHVYIPEAEKA---GIIRYAIQVGDAREPPTALQELMTIGSAPQDHYF 315
 QY 200 PVDGFOALQGIHSLKSCIEILAEPSITCAGESFOVYVVRNGFPHARVD 253

Db 316 KVGN-FVALRSIQIOIEK-----IFAIGTESRSSSSFHHEMSQEGFSSALSMD 364

RESULT 11

US-08-362-652-53
; Sequence 53, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,652
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-362-652-53

Query Match 9.6%; Score 166; DB 1; Length 1161;

Best Local Similarity 28.2%; Pred. No. 3.4e-09; Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GPDLYFIIDKGSV-LHMHNEIYFVEQLAKFISPOLMSFIYVSTGTLMK 94
Db 144 PECGQEMDI AFLIDGSGSIDQSDFTQKDFVKALMGQLASTSTSFSLMOYSNLKTHFT 203
Qy 95 LTERD-----EQIQGLEBLQKVLPGDVTWHEGFERASEQIYENRGYRTA-SVITAL 148
Db 204 FTEFKSLSPQSLDAIVQLQ-----GLTYTASGIQVKVKELFHSGKARKSAKKILIVI 258
Qy 149 TDGELHDLFEYSE--REANRSRDIGATVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
Db 259 TDGQKFRDPLEYRHVYIEAEKA--GIRYALGVGDAPREPTALQELNTIGSAPSQDHVF 315
Qy 200 PVNDGFALQGIHSLKKSCTEILAAEPSTICAGESFOVVVRGNGFRHARNVD 253
Db 316 KVGN-FVALRSIQIOIEK-----IFAIGTESRSSSSFHHEMSQEGFSSALSMD 364

RESULT 12

US-08-605-672-53
; Sequence 53, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-605-672-53

Query Match 9.6%; Score 166; DB 2; Length 1161;

Best Local Similarity 28.2%; Pred. No. 3.4e-09; Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GPDLYFIIDKGSV-LHMHNEIYFVEQLAKFISPOLMSFIYVSTGTLMK 94
Db 144 PECGQEMDI AFLIDGSGSIDQSDFTQKDFVKALMGQLASTSTSFSLMOYSNLKTHFT 203
Qy 95 LTERD-----EQIQGLEBLQKVLPGDVTWHEGFERASEQIYENRGYRTA-SVITAL 148
Db 204 FTEFKSLSPQSLDAIVQLQ-----GLTYTASGIQVKVKELFHSGKARKSAKKILIVI 258
Qy 149 TDGELHDLFEYSE--REANRSRDIGATVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
Db 259 TDGQKFRDPLEYRHVYIEAEKA--GIRYALGVGDAPREPTALQELNTIGSAPSQDHVF 315
Qy 200 PVNDGFALQGIHSLKKSCTEILAAEPSTICAGESFOVVVRGNGFRHARNVD 253
Db 316 KVGN-FVALRSIQIOIEK-----IFAIGTESRSSSSFHHEMSQEGFSSALSMD 364

RESULT 13

US-08-482-293A-53
; Sequence 53, Application US/08482293A

Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-53

Query Match 9.6%; Score 166; DB 2; Length 1161;
Best Local Similarity 28.2%; Pred. No. 3.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GPDLYFLDKSGSV-LHNNELIYFVEQLAHKFIISPOLMSPFVSTRTITLMK 94
DB 144 PECPOEMDIADFLDGSISIDSDPTQMKDFKALMGQLASTSTFSIMQYSNILKHTPT 203
QY 95 LTEDR-----EQIRGLELQVLPFGDTYHMEGPERASEQIYENRGYRTA-SVITAL 148
DB 204 FTEFKSSISPSGLVDALVQLQ-----GLTYTASGIQKVKELFHSKNARKSAAKILIVI 258
QY 149 TDGEIHEDLFFYSR--REANRSRDGAIVYCVGVD-FNE-TQLARI-----ADSKDHYF 199
DB 259 TDGQKFRDPLEYRAHYIPEAKA---GIIRYAIQVGDAREPTALQELNTIGSAPSDHYF 315
QY 200 PYNDGFQALQGIHILKKSCEILAAEPSTICAGESFQVVRGNGFRHARVD 253
DB 316 KVGN-FVALRSIQRIQIERK---IFAIGTESRSSSSSFQHEMSQGFSSALSM 364

RESULT 14
US-08-943-363-53
Sequence 53, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-53

Query Match 9.6%; Score 166; DB 2; Length 1161;
Best Local Similarity 28.2%; Pred. No. 3.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GPDLYFLDKSGSV-LHNNELIYFVEQLAHKFIISPOLMSPFVSTRTITLMK 94
DB 144 PECPOEMDIADFLDGSISIDSDPTQMKDFKALMGQLASTSTFSIMQYSNILKHTPT 203
QY 95 LTEDR-----EQIRGLELQVLPFGDTYHMEGPERASEQIYENRGYRTA-SVITAL 148
DB 204 FTEFKSSISPSGLVDALVQLQ-----GLTYTASGIQKVKELFHSKNARKSAAKILIVI 258
QY 149 TDGEIHEDLFFYSR--REANRSRDGAIVYCVGVD-FNE-TQLARI-----ADSKDHYF 199
DB 259 TDGQKFRDPLEYRAHYIPEAKA---GIIRYAIQVGDAREPTALQELNTIGSAPSDHYF 315
QY 200 PYNDGFQALQGIHILKKSCEILAAEPSTICAGESFQVVRGNGFRHARVD 253
DB 316 KVGN-FVALRSIQRIQIERK---IFAIGTESRSSSSSFQHEMSQGFSSALSM 364

RESULT 15
US-09-193-043-53
Sequence 53, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica

; TITLE OF INVENTION: No. 6251395e1 Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 1161
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-193-043-53

Query Match 9.6%; Score 166; DB 3; Length 1161;
Best Local Similarity 28.2%; Pred. No. 3,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLDKSGSV-LHWNELIYFVEQLAHKFI SPQLMSFIVFSTRGTTLMK 94
Db 144 PECPQEMDIAFLIDSGSIDQSDFTQMKDFYKALMGQLASTSTSFSLMOYSNLIKTHFT 203
Qy 95 LTEDR-----EIRQGLEELQKVLPGDPTVMHEGFERASEQIYYENRQGRTA-SVITAT 148
Db 204 FTEFKSSLSPOSVDATVQLQ----GLTYTASGIQKVKELFHSKNGARKSAKKILIVI 258
Qy 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVGVKD-FNE--TOLARI-----ADSKDHVF 199
Db 259 TDGQKFRPRLERHRYTPAEKA---GIRYALGVDAFREPTALQELNTTIGSAPSQDHVF 315
Qy 200 PVNDGFQALQGIHSHILKSCIEIILAEPSTICAGESFQVVVRNGGFRHARND 253
Db 316 KVGN-FVALRSTIQRIQEK---IPALRGTESRSSSSSFQHEWSQEGFSALSM 364

Search completed: June 21, 2004, 13:46:36
Job time : 13.5745 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:39:51 / Search time 21.2974 Seconds
(without alignments)
1367.166 Million cell updates/sec

Title: US-09-970-076-6

Perfect score: 3025

Sequence: 1 MATARRALGICFQWLSLAT.....QAPPNNRAPPSRPPRSV 564

Scoring table: BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	6.6	104	4 US-09-547-693-235	Sequence 235, App
2	191.5	6.3	306	1 US-08-217-327-6	Sequence 6, Appl
3	186	6.1	76	4 US-09-547-693-233	Sequence 233, App
4	186	6.1	214	1 US-08-217-327-4	Sequence 4, Appl
5	173.5	5.7	142	4 US-09-252-991A-24873	Sequence 24873, A
6	173.5	5.7	334	6 5202236-3	Patent No. 5202236
7	171.5	5.7	331	6 5202236-37	Patent No. 5202236
8	167.5	5.5	1248	2 US-09-080-897-2	Sequence 2, Appl
9	167.5	5.5	1248	3 US-09-323-735-2	Sequence 2, Appl
10	167	5.5	1231	4 US-08-714-741-41	Sequence 41, Appl
11	166	5.5	1155	1 US-08-286-889-46	Sequence 46, Appl
12	166	5.5	1155	1 US-08-485-618-46	Sequence 46, Appl
13	166	5.5	1155	1 US-08-362-652-46	Sequence 46, Appl
14	166	5.5	1155	2 US-08-605-672-46	Sequence 46, Appl
15	166	5.5	1155	2 US-08-482-293A-46	Sequence 46, Appl
16	166	5.5	1155	2 US-08-943-363-46	Sequence 46, Appl
17	166	5.5	1155	4 US-09-193-043-46	Sequence 46, Appl
18	166	5.5	1155	4 US-09-688-307A-46	Sequence 46, Appl
19	166	5.5	1155	4 US-09-350-259-46	Sequence 46, Appl
20	166	5.5	1161	1 US-08-485-618-53	Sequence 53, Appl
21	166	5.5	1161	1 US-08-362-652-53	Sequence 53, Appl
22	166	5.5	1161	2 US-08-605-672-53	Sequence 53, Appl
23	166	5.5	1161	2 US-08-482-293A-53	Sequence 53, Appl
24	166	5.5	1161	2 US-08-943-363-53	Sequence 53, Appl
25	166	5.5	1161	3 US-09-193-043-53	Sequence 53, Appl
26	166	5.5	1161	4 US-09-688-307A-53	Sequence 53, Appl
27	166	5.5	1161	4 US-09-350-259-53	Sequence 53, Appl

28	165	5.5	105	4 US-09-547-693-230	Sequence 230, App
29	163	5.4	635	1 US-07-832-855-2	Sequence 2, Appl
30	162.5	5.4	203	4 US-09-543-681A-8287	Sequence 8287, Ap
31	162	5.4	559	4 US-10-116-370-2	Sequence 2, Appl
32	161.5	5.3	1315	3 US-08-899-595-3	Sequence 3, Appl
33	161	5.3	72	4 US-09-547-693-231	Sequence 231, App
34	160.5	5.3	1255	2 US-09-080-897-4	Sequence 4, Appl
35	160.5	5.3	1255	3 US-08-899-595-1	Sequence 1, Appl
36	160.5	5.3	1255	3 US-09-323-735-4	Sequence 4, Appl
37	159.5	5.3	503	4 US-09-599-287A-2	Sequence 2, Appl
38	159.5	5.3	1151	1 US-08-286-889-37	Sequence 37, Appl
39	159.5	5.3	1151	1 US-08-485-618-37	Sequence 37, Appl
40	159.5	5.3	1151	1 US-08-362-652-37	Sequence 37, Appl
41	159.5	5.3	1151	2 US-08-605-672-37	Sequence 37, Appl
42	159.5	5.3	1151	2 US-08-482-293A-37	Sequence 37, Appl
43	159.5	5.3	1151	2 US-08-943-363-37	Sequence 37, Appl
44	159.5	5.3	1151	3 US-09-193-043-37	Sequence 37, Appl
45	159.5	5.3	1151	4 US-09-688-307A-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-547-693-235
; Sequence 235, Application US/09547693
; Patent No. 6639050
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/09/547,693
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
US-09-547-693-235

Query Match 6.6%; Score 199; DB 4; Length 104;
Best Local Similarity 47.5%; Pred. No. 4.2e-10;
Matches 38; Conservative 7; Mismatches 33; Indels 2; Gaps 1;

QY 485 TRVKNQPAKTYLNNAYHTSSPPAPITTPPPAPHCPPPPSAFTPTPPSTLP--P 542
DB 4 TRASPPSP 63
QY 543 PPOAPPNNRAPPSRPPSP 562
DB 64 PPSPPSPSPSPSPSPSPSP 83

RESULT 2
US-08-217-327-6
; Sequence 6, Application US/08217327
; Patent No. 5474925
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E
; TITLE OF INVENTION: Barton, Kenneth A
; TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Quarles and Brady
; STREET: P. O. Box 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA

ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 1122990831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-217-327-6

Query Match 6.1%; Score 191.5; DB 1; Length 306;
Best Local Similarity 26.1%; Pred. No. 9e-09;
Matches 59; Conservative 18; Mismatches 56; Indels 93; Gaps 10;

Qy 352 KEVPP---PAEESSEEDDDGLPKKQWPTVDASYGGRGVGIGIKMEVMEKSTEGS 408
Db 144 KSPPPKSPAPENHYTKKSPPPKHPAPENHY----- 177
Qy 409 KLEKAKNARYVMEQGEYFPEPRRLNNMRRSPSPKWSPIKGLDALWYLKRGYDRV 468
Db 178 -KYKKSPPPPTPVYKYSPP-----PTPVYKYSKSP----- 208
Qy 469 SVMRQPDGTGRCLNFTVKANNQPAKYPLNNAHYTSSPPAPITYPPPAHCPPPPP-- 526
Db 209 ---PPP-----KISPA--PVNHKKYKSPPPPTPVYKYSPPPPHSPPPPTPV 249
Qy 527 ---SAPTPPIPSPTLPPPP-----QAPPPRAPP--GRPPR 561
Db 250 YKYSPPPPMHSPP---PPTPVYKYSPPPPMHSPPPPVYSPPPPK 292

RESULT 3
US-09-547-693-233
Sequence 233, Application US/09547693
Patent No. 6639050
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 233
LENGTH: 76
TYPE: PRT
ORGANISM: Artificial/Unknown
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
US-09-547-693-233

Query Match 6.1%; Score 186; DB 4; Length 76;
Best Local Similarity 56.2%; Pred. No. 3.7e-09;

Matches 36; Conservative 6; Mismatches 18; Indels 4; Gaps 3;
Qy 505 SPPAPITYPPAPACPP--PPPSATPPIPSPTLPP--POAPPNNAP--PPSRPP 560
Db 12 SPPSP 71
Qy 561 RPSV 564
Db 72 SPSM 75

RESULT 4
US-08-217-327-4
Sequence 4, Application US/08217327
Patent No. 5474925
GENERAL INFORMATION:
APPLICANT: John, Mallyakal E
APPLICANT: Barton, Kenneth A
TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles and Brady
STREET: P.O. Box 2113
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 1122990831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-217-327-4

Query Match 6.1%; Score 186; DB 1; Length 214;
Best Local Similarity 47.0%; Pred. No. 1.7e-08;
Matches 39; Conservative 5; Mismatches 23; Indels 16; Gaps 4;

Qy 496 PLNNAHYTSSPPA-----PIYTPPP--PAFHCPP--PPSAPTPPIPSPTLPP----- 542
Db 60 PVSTPPPTSSPPPTVDSPPVSTPPSPSPSPAPATPPASPPATPPASPPATPPASPP 119
Qy 543 ---PPOAPPNNRAPPPSPPPRP 562
Db 120 PATPPATPPATPPATPPAP 142

RESULT 5
US-09-252-991A-24873
Sequence 24873, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24873
LENGTH: 142
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24873

Query Match 5.7%; Score 173.5; DB 4; Length 142;
Best Local Similarity 53.7%; Pred. No. 1.2e-07;
Matches 36; Conservative 7; Mismatches 15; Indels 9; Gaps 5;

QY 506 PPAPITYPPPPAPHCPP-----PPSAFTPTPI-PSPESTLPP-PQAPPPNRP--PPSR 557
Db 66 PPPSPSPSPPPPPPPPPVPPVPPSPPPVPPSPPPPPPPPPPPPPPPPPPPPPPPPPPP 125

QY 558 P-PPRPS 563
Db 126 PGPPSPS 132

RESULT 6
5202236-3
PATENT NO. 5202236
APPLICANT: MUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,
SUSAN L.; MCCANDLIS, RUSSELL; TENA, FILIPULA, DAVID
TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
PROTEIN
NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
SEQ ID NO: 3;
LENGTH: 334
5202236-3

Query Match 5.7%; Score 173.5; DB 6; Length 334;
Best Local Similarity 51.6%; Pred. No. 4e-07;
Matches 33; Conservative 4; Mismatches 16; Indels 11; Gaps 3;

QY 507 PPAPITYPP-----PAPHCPPPPPSAPPTPIPSPESTLPPPPQAPPPNRPAPPPSRP 558
Db 8 PPAPAFAPALAPAPNPNNPQSPSPSPPTTP--PPAPSPSPSPPPPPPPSP 64

QY 559 PPRP 562
Db 65 PPSP 68

RESULT 7
5202236-37
PATENT NO. 5202236
APPLICANT: MUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,
SUSAN L.; MCCANDLIS, RUSSELL; TENA, FILIPULA, DAVID
TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
PROTEIN
NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762

FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
SEQ ID NO: 37;
LENGTH: 331
5202236-37

Query Match 5.7%; Score 171.5; DB 6; Length 331;
Best Local Similarity 51.6%; Pred. No. 5.9e-07;
Matches 33; Conservative 4; Mismatches 16; Indels 11; Gaps 3;

QY 507 PPAPITYPP-----PAPHCPPPPPSAPPTPIPSPESTLPPPPQAPPPNRPAPPPSRP 558
Db 5 PPAPAFAPALAPAPNPNNPQSPSPSPPTTP--PPAPSPSPSPPPPPPPSP 61

QY 559 PPRP 562
Db 62 PPSP 65

RESULT 8
US-09-080-897-2
Sequence 2, Application US/09080897
PATENT NO. 5985574
GENERAL INFORMATION:
APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
APPLICANT: Morrow, Jan E.
APPLICANT: Welch, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,897
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-080-897-2

Query Match 5.5%; Score 167.5; DB 2; Length 1248;
Best Local Similarity 35.5%; Pred. No. 9e-06;
Matches 43; Conservative 3; Mismatches 20; Indels 55; Gaps 6;

QY 473 PQPDGTGRCINFTRVKNQNPAPKYPLNNAVHTSSPPAP--IYTPPPAPHCPPPP----- 526

Db 578 PLPGDSGTII-----PPPPAGDSTPPPPPPPPPPPLPG 615
Qy 527 -----SAPPP-----IPSPS-----TLPPPAQAPPNRAAPPSRPPR 561
Db 616 TAISPPPLSGDATIPPPPLPGVGIPSPSLPGCTAIPPPPLPGSARIPPP--PPPL 673
Qy 562 P 562
Db 674 P 674

RESULT 9
US-09-323-735-2
; Sequence 2, Application US/09323735
; Patent No. 6197932
; GENERAL INFORMATION:
; APPLICANT: King, Mary-Claire
; APPLICANT: Lynch, Eric D.
; APPLICANT: Lee, Ming
; APPLICANT: Morrow, Jan E.
; APPLICANT: Welch, Piri L.
; APPLICANT: Leon, Pedro E.
; TITLE OF INVENTION: Modulators of Actin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/323,735
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/080,897
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UM97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-323-735-2

Query Match 5.5%; Score 167.5; DB 3; Length 1248;
Best Local Similarity 35.5%; Pred. No. 9e-06;
Matches 43; Conservative 3; Mismatches 20; Indels 55; Gaps 6;

Qy 473 POPGDTGRCINFRKNNQAPKYPLNNAYHTSSPPAP--ITYPPPAHQPPPP----- 526
Db 578 PLPGDSGTII-----PPPPAGDSTPPPPPPPPPPPLPG 615
Qy 527 -----SAPPP-----IPSPS-----TLPPPAQAPPNRAAPPSRPPR 561
Db 616 TAISPPPLSGDATIPPPPLPGVGIPSPSLPGCTAIPPPPLPGSARIPPP--PPPL 673
Qy 562 P 562

Db 674 P 674

RESULT 10
US-08-714-741-41
; Sequence 41, Application US/08714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edw'n
; APPLICANT: Yotner, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,741
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1231 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; US-08-714-741-41

Query Match 5.5%; Score 167; DB 4; Length 1231;
Best Local Similarity 31.4%; Pred. No. 9.8e-06;
Matches 54; Conservative 16; Mismatches 72; Indels 30; Gaps 7;

Qy 400 EKSTEEGAKLEKRAKNRVKQPEQVEYFPP-----ENLNNMRR--PSSPRKYSPIKG 452
Db 565 EKTAEKKALEKAE-ADLKAVDEPPTAPAPQKAAEENNNVVDYRKEGLEKTIKKA 623
Qy 453 KLDALWLLRKGYDRVSVMRPQPGDTGRCINFRKNNQAPKYPLNNAYHTSSPPAPYI 512
Db 624 ELEKTEADLKAVVEPEKPAAP-----EPAPAEKPA-----EKPAAP-- 663
Qy 513 TTPPPAHCPPPPSAPTPPIPS--PSTLPPPAQAPPNRAAPPSRPPR 562
Db 664 EKPAAPAEKPAPEKPAAPATPAEAPAEQPKAPAPQAPAPPEKPAQOP 715

RESULT 11
US-08-286-889-46
; Sequence 46, Application US/08286889
; Patent No. 5470953

```

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-46

Query Match 5.5%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-05;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GFDLYFLDKSGSV-LHNNELIYFVEQLAHKFISPOLMSFIVSTRGTTLMK 94
DB 144 PECQEQEMDIAPLDIGSSSIDQSDPTQMKDFVKALMGQLASTSTSFSLMQYSNLIKHTFT 203
QY 95 LTEDR-----EQIRQGLELQKVLPGDPTVMHEGFERASEQIYYENRCGYRTA-SVITL 148
DB 204 FTEFSSLSPOSTLVDAIVQLQ-----GLTYTASGIQKVKELFHSKNGARKSAKKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 199
DB 259 TDGQKFRDPLRYRHVYIPEAKA---GIIRYALGVGDARFEPALQELMTIGSAPQDHVF 315
QY 200 PVNDGFOLQGIHSHILKXSCIEILAEPSITCAGESFQVVRNGGFRHARNVD 253
DB 316 KVG-N-FVALRSIORIOEK---IFALIGTESRSSSFQHEMSQGFSSALSMD 364

RESULT 12
US-08-485-618-46
Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
```

```

CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-46

Query Match 5.5%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-05;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GFDLYFLDKSGSV-LHNNELIYFVEQLAHKFISPOLMSFIVSTRGTTLMK 94
DB 144 PECQEQEMDIAPLDIGSSSIDQSDPTQMKDFVKALMGQLASTSTSFSLMQYSNLIKHTFT 203
QY 95 LTEDR-----EQIRQGLELQKVLPGDPTVMHEGFERASEQIYYENRCGYRTA-SVITL 148
DB 204 FTEFSSLSPOSTLVDAIVQLQ-----GLTYTASGIQKVKELFHSKNGARKSAKKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 199
DB 259 TDGQKFRDPLRYRHVYIPEAKA---GIIRYALGVGDARFEPALQELMTIGSAPQDHVF 315
QY 200 PVNDGFOLQGIHSHILKXSCIEILAEPSITCAGESFQVVRNGGFRHARNVD 253
DB 316 KVG-N-FVALRSIORIOEK---IFALIGTESRSSSFQHEMSQGFSSALSMD 364
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```

RESULT 13
US-08-362-652-46
Sequence 46, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
```

COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-46

Query Match 5.5%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-05;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYG-GPDIYFIDKSGSV-LHHMNEIYYFVEQLAHKFIISPOLRMSPIVSTRTGLMK 94
DB 144 PECQGEQMDIAFLDGSISIDQSDPTQKDFVKALMGQLASTSTSPSLMOYSNLKTHFT 203
QY 95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHGEGFERASQIYYENRGYRTA-SVIAL 148
DB 204 FTEKSSLSPOSIDVAIVOLQ-----GLTYASGIQKVKELFHSKNGARKSAKKILIVI 258
QY 149 TDGELHEDLFYYSR--REANRSRLGAIYVCVGVKD-FNE-TOLARI-----ADSKDHF 199
DB 259 TDGQKRPDPLEYRNHVIPEAKA---GIRYALGVGDARFEPYALQELNTTGSAPSQDHVF 315
QY 200 PVNDGFQALQGIHSLKSCIEILAEPSITCAGESFOVVVRGNGFRHARNVD 253
DB 316 KVGN-FVALRSIQROIQEK---IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 14
US-08-605-672-46
Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-46

Query Match 5.5%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-05;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYG-GPDIYFIDKSGSV-LHHMNEIYYFVEQLAHKFIISPOLRMSPIVSTRTGLMK 94
DB 144 PECQGEQMDIAFLDGSISIDQSDPTQKDFVKALMGQLASTSTSPSLMOYSNLKTHFT 203
QY 95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHGEGFERASQIYYENRGYRTA-SVIAL 148
DB 204 FTEKSSLSPOSIDVAIVOLQ-----GLTYASGIQKVKELFHSKNGARKSAKKILIVI 258
QY 149 TDGELHEDLFYYSR--REANRSRLGAIYVCVGVKD-FNE-TOLARI-----ADSKDHF 199
DB 259 TDGQKRPDPLEYRNHVIPEAKA---GIRYALGVGDARFEPYALQELNTTGSAPSQDHVF 315
QY 200 PVNDGFQALQGIHSLKSCIEILAEPSITCAGESFOVVVRGNGFRHARNVD 253
DB 316 KVGN-FVALRSIQROIQEK---IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 15
US-08-482-293A-46
Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-46

Query Match 5.5%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-05;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

OY 37 PACTG-GFDLYFILDKSGSV-LHWNIEIYFVEQLAHKFIPOQMSPIVSTGTTLMK 94
DB 144 PECFQEMDIAPFLIDSGSIDQSDFTQMKDFKALMGQLASTSTSPSLMOYSNLIKTHFT 203
OY 95 LTEDR-----EQIRGLLELOKVLPGDPTMHGFEFASSEQIYENRQGYRTA-SVITL 148
DB 204 FTERKSSLSPOSVDIVQLQ-----GLYITASGIQVVKELFHKNQARKSAKKILIVT 258
OY 149 TDGELHEDLFPYSE--REANRSRDLAGIYVCVVD-FNE-TOLARI-----ADSKDHVF 199
DB 259 TDGQKFRDPLEYRHVYIPEAKA---GIRVAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
OY 200 PVNDGFALQGIHISILKKSCTEIIAABPTICAGESFOVVVRGNGFRHARNVD 253
DB 316 KVGN-FVALRSIQRIQIEK---IPALGTESRSSSSFOHEMSQEGFSSALSM 364

Search completed: June 21, 2004, 13:46:35
Job time : 22.2974 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 22, 2004, 02:37:46 ; Search time 840.105 Seconds

(without alignment)
3075.489 Million cell updates/sec

Title: US-09-970-076-6
Perfect score: 3025
Sequence: 1 MATERRALGICFQWLSLAT.....QAPPPNRAPPSRPPRRSV 564

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEVEXLH
-Q=/cg2_1/USPFO_epool/US09970076/runac_21062004.125533.8805/app_query.fasta_1.2140
-DB=Published Applications NA -QPM=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blowsum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=spc -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=100000000 -USER=US09970076 -CGEN_1_1_1225 @runac_21062004.125533.8805
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cg2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cg2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
3: /cg2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
4: /cg2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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16: /cg2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
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18: /cg2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
19: /cg2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
------------	-------------	-------	--------	----	-------------

1	3025	100.0	5540	13	US-09-918-715-176	Sequence 176, App
2	3025	100.0	5540	13	US-09-918-715-231	Sequence 231, App
3	3025	100.0	5540	15	US-10-301-822-198	Sequence 198, App
4	2901	95.9	5220	13	US-09-918-715-186	Sequence 186, App
5	2901	95.9	5220	13	US-09-918-715-300	Sequence 300, App
6	2022	66.8	3981	13	US-10-302-172-250	Sequence 250, App
7	2017	66.7	4417	10	US-09-796-753-23	Sequence 23, App
8	2017	66.7	4417	15	US-10-038-107-3	Sequence 3, App
9	2017	66.7	4417	15	US-10-201-292-1	Sequence 3, App
10	1894	62.6	1454	16	US-10-133-317-58	Sequence 38, App
11	1894	62.6	1454	16	US-10-159-563-58	Sequence 58, App
12	1661	54.9	1674	15	US-10-038-107-17	Sequence 17, App
13	1661	54.9	1674	15	US-10-201-292-15	Sequence 15, App
14	1652.5	54.6	1650	15	US-10-038-107-15	Sequence 15, App
15	1652.5	54.6	1650	15	US-10-201-292-15	Sequence 15, App
16	1650.5	54.6	1650	15	US-10-038-107-13	Sequence 13, App
17	1650.5	54.6	1650	15	US-10-201-292-13	Sequence 13, App
18	1650	54.5	2272	10	US-09-796-753-11	Sequence 11, App
19	1650	54.5	2272	15	US-10-038-107-1	Sequence 1, App
20	1650	54.5	2272	15	US-10-201-292-1	Sequence 1, App
21	1650	54.5	2353	15	US-10-198-846-9957	Sequence 9957, App
22	1650	54.5	2459	9	US-09-833-381-998	Sequence 998, App
23	1649	54.5	1056	15	US-10-038-107-23	Sequence 23, App
24	1649	54.5	1056	15	US-10-201-292-23	Sequence 23, App
25	1649	54.5	1056	15	US-10-038-107-19	Sequence 19, App
26	1649	54.5	1713	15	US-10-201-292-19	Sequence 19, App
27	1640.5	54.2	1650	15	US-10-038-107-9	Sequence 9, App
28	1640.5	54.2	1650	15	US-10-201-292-9	Sequence 9, App
29	1636	54.1	1008	15	US-10-038-107-25	Sequence 25, App
30	1636	54.1	1008	15	US-10-201-292-25	Sequence 25, App
31	1634.5	54.0	1047	15	US-10-038-107-21	Sequence 21, App
32	1634.5	54.0	1047	15	US-10-201-292-21	Sequence 21, App
33	1557.5	51.5	1608	15	US-10-201-292-35	Sequence 35, App
34	1530	50.6	2397	16	US-10-062-674-1757	Sequence 1757, App
35	1509.5	49.9	1623	15	US-10-038-107-11	Sequence 11, App
36	1509.5	49.9	1623	15	US-10-201-292-11	Sequence 11, App
37	1423	47.0	2334	15	US-10-104-047-669	Sequence 669, App
38	1416.5	46.8	2234	16	US-10-368-087-9	Sequence 9, App
39	1416.5	46.8	4081	15	US-09-796-753-51	Sequence 51, App
40	1411.5	46.7	3677	15	US-10-038-107-5	Sequence 5, App
41	1411.5	46.7	3677	15	US-10-201-292-5	Sequence 5, App
42	1411.5	46.7	3677	15	US-10-038-107-5	Sequence 5, App
43	1411.5	46.7	3677	15	US-10-201-292-5	Sequence 5, App
44	1396.5	46.2	3501	10	US-09-814-353-22000	Sequence 22000, App
45	1396.5	46.2	3501	10	US-09-796-753-53	Sequence 53, App
					US-10-038-107-7	Sequence 7, App

ALIGNMENTS

RESULT 1
US-09-918-715-176
; Sequence 176, Application US/09918715
; Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
TITLE OF INVENTION: ENDOGENOUS CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918, 715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 5540
TYPE: DNA

ORGANISM: Homo sapiens
US-09-918-715-176

Alignment Scores:
Pred. No.: 8,21e-284 Length: 5540
Score: 3025.00 Matches: 564
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-970-076-6 (1-564) x US-09-918-715-176 (1-5540)

1 MetAlATrAlAGlUArGAlAlAuGlylIleGIPheGInTPLeuSerIleuAlaThr 20
144 ATGGCCAGCGGAGGAGAGCCCTCGGCATCGGCTTCAAGTGGCTCTTGGCCACT 203
QY 21 LeuValIleuIleCyAlAGlyGInGlylYArGArGluAPrGlyGlyProAlaCyArY 40
Db 204 CTGGGTCTCATCTCGCGCGGCAAGCGGAGCGCAAGAGATGGGGGTCCAGCTGTAC 263
QY 41 GlyGlyPheAPrLeuTYrPheIleuAPrIySerGlySerValIleuHisITrAsn 60
Db 264 GACGATTTGACCTGTACTCTCATTTTGGACAAATCAGAAAGTGTGTCCACCACTGAAAT 323
QY 61 GluIleTYrTYrPheValIGluGInIleuAlaHisIyPheIleSerProGInIleuArGMet 80
Db 324 GAATCTATTACTTGTGGACAGTGTGCTCAAAATTCATCAGCCCACTGAGAAATG 383
QY 81 SerPheIleValPheSerThrArGlyThrThreuMetIySleuThrGluAPrArGlu 100
Db 384 TCTTTATTGTCTTCCACCGGAGAAACCTTAATGAAATGAAACAGAAAGACAGAA 443
QY 101 GInIleArGInGlyIleuGluGInIleuValIleuProGlyGlyArPThrTYrMet 120
Db 444 CAATTCCTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGGAGAGACACTTACATG 503
QY 121 HisGluGlyPheGluArGAlAserGluGInIleTYrTYrGluAPrArGInGlyTYrArG 140
Db 504 CATGAAGATTTGAAAGGCGCAGTGAAGCAATTTATTTGAAACAGCAAGGAGTACAG 563
QY 141 ThrAlaSerValIleIleAlaIleuThrAPrGlyIleuHisIySleuAPrPhePheTYr 160
Db 564 ACAGCAGACGTCATCATTTGCTTGTGACTGATGAGAACTCCATGAAGATCTTTTTCAT 623
QY 161 SerGluArGAlaAlaAPrArGArSerArPheIleuGlyAlIleValTYrCyValAlGlyAl 180
Db 624 TCAAGAGAGGAGGCTAATAGTCTCGAATCTTGTGCAATTTGTTACTGTGTGTGTG 683
QY 181 LysAPrPheAPrGluThrGInIleuAlaArGIIeAlaAPrSerIyAsAPrHisValPhePro 200
Db 684 AAAAGTTTCATGAGACACAGCTGCGCGGANTGGGCAAGTGAAGATCATGTGTTC 743
QY 201 ValIleAPrGlyPheGInAlaIleuGInGlyIleIleHiserIleuIySleuSerCyS 220
Db 744 GTGATGACGCGCTTTCAGGCTCTCGCAAGGCAATCATCTCAATTTTGAAGAGCTCCG 803
QY 221 IleguIleuAlaIleGluProSerThrIleCyAlAGlyGInSerPheGInValAl 240
Db 804 ATCGAAATTTCAAGCAGTGAACCACTCCCAATATGAGAGAGACTCATTTCAAGTTTC 863
QY 241 ValArGAlAsnGlyPheArGHisAlaArGArValAPrArGValIleuCySerPheIyS 260
Db 864 GTGAGAGGAAACGCTTCCGACATCCCGCAACGTGACAGGCTCTTCCAGCTTCAAG 923
QY 261 IleAPrAPrSerValThreuAPrGluIyPheProPheSerValGluAPrThrTYrIleu 280
Db 924 ATCATATGACTCGGTCACTCATATGAGAAAGCCCTTTCTGTGAGAGATATTATTACTG 983
QY 281 CysProAlaProIleuIyGluIyAlGlyMetIySAlaAlaIleuGInValSerMetAsn 300
Db 984 TGTCCAGGCGCTCATCTTAAAGAAAGTGTGCAATGAAGAGCTCCAGGTCAAGCATGAAC 1043

QY 301 AspGlyLeuSerPheIleSerSerValIleIleThrThrHisCySerSerAspGly 320
Db 1044 GATGGCTCTCTTTTATCTCCAGTTCTGTATATGACCAACACACTGTGTGACGGT 1103
QY 321 SerIleuAlaIleAlaIleuIleuPheIleuIleuAlaIleuIleuTrp 340
Db 1104 TCCATCTCGGCAATCGGCTCGTGAATCTGTCTCTGCTGAGCCCTGCTCTCGG 1163
QY 341 TrpPheTrpProIleuCySthrValIleIleIySleuValProProProAlaGlu 360
Db 1164 TGGTTCTGGCCCCCTCTCTGCTGCTGATTTATCAAGAGTCCCTCCACCCCTGGAG 1223
QY 361 GluSerGluGluIleuAPrAPrGlyIleuProIyAlSlySTPProThrValAspAla 380
Db 1224 GAGAGTAGAGAAAGATGATGATGTGTGCTGTCAAGAAAGTGGCCAAACGCTGAGCC 1283
QY 381 SerTYrTYrGlyIyAlGlyIyAlGlyIyIleIyArGMetGluValArGTTrGlyGlu 400
Db 1284 TCTTATTATGTGTGGAGAGCGGTGGAGCATTTAAAGAAATGGAGTTCTGTGGGAGAA 1343
QY 401 LysGlySerThrGluGluGluIyAlaIySleuGluIySAlaIyAsAPrAlaArGValIyMet 420
Db 1344 AAGGCTCCACAGAAAGAGTGTCTAATTTGAAAGGCAAGAAATGCAAGATCAAGATG 1403
QY 421 ProGluGInIyTYrGluPheProGluProArGAsnIleuAsnAPrArGArGPro 440
Db 1404 CCGAGAGAGAAATATGAAATTCCTGAGCCGGAATCTCAACAAATATATCGTCCGCT 1463
QY 441 SerSerProArGlySTPTYrSerProIleIySleuIySleuAPrAlaIleUTrValIleu 460
Db 1464 TCTTCCCCCGGAAGTGTACTCTCAATCAAGGAAATCGATGCTGTGGGTCTTA 1523
QY 461 LeuArGlySlyTYrArAPrArGValSerValIleArGProGInPProGlyArPThrGlyArG 480
Db 1524 CTGAGAAAGATATGATCTGTGTCTGTATGCTGCACAGCCAGAGAGACCGGGCGC 1583
QY 481 CysIleAsnPheThrArGValIyAsnAsnGInProAlaIySTYrProIleuAsnAla 500
Db 1584 TGCATCAATTTCAACAGAGGTCAAGAAACACAGCAGCAAGTATCCACTCAACAGCC 1643
QY 501 TyrHisThrSerSerProProProAlaProIleTYrThrProProProProAlaProHis 520
Db 1644 TACCAACCTCTCTCGCGCTCTCGCCCACTCACTCACTCCCACTCTCGCCGCCAC 1703
QY 521 CysProProProProSerAlaProThrProProIleProSerProProSerThre 540
Db 1704 TGCCCTCCCCCGCCCCAGGCGCCCTTACCCTCCATCCGATCCCACTTCCACCTT 1763
QY 541 ProProProProGInAlaProProProAsnArGAlaProProProSerArGProPro 560
Db 1764 CCCCCTCTCCCGAGGCTCCACCTCCCAAGGGCACCTCTCCCTCCGCGCTCTCCA 1823
QY 561 ArgProSerVal 564
Db 1824 AGGCTTCTGTG 1835

RESULT 2
US-09-918-715-231
; Sequence 231, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850

APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MEM01-0292PRNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 198
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (144)... (1838)
US-10-301-822-198
Alignment Scores:
Pred. No.: 8,21e-284 Length: 5540
Score: 3025.00 Matches: 564
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-09-970-076-6 (1-564) x US-10-301-822-198 (1-5540)
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Db 144 ATGGCCACGGCGGAGCGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 203
QY 21 LeuValLeuIleCysAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysPyr 40
Db 204 CTGGGCTCATCTGCGCGGAGGAGGAGCGACGAGAGAGAGGAGGCTGCTAC 263
QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrrAsn 60
Db 264 GCGGATTTGACCTGACTTCTTTCGACAAATCAGAAAGTCTGACACCTGAT 323
QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
Db 324 GAAATCTATTACTTTGTGGACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db 384 TCTTTATTGTTTCTCCACCGAGAGAACCTTAAATGAAATCAGAAAGACAGAA 443
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db 444 CAATCCGTCAGAGCGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 503
QY 121 HisGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
Db 504 CATGAGAGATTGGAAGGCGCAGTAGCAGATTATTATGAAACAGACAAAGGATACAG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160
Db 564 ACAGCAGAGCTATATTGCTTGTGACTAGTAGAGAACTCCAGAAAGATCTTTTCTAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValIleTyrCysValGlyVal 180
Db 624 TCAGAGAGAGAGGCTTAAATGCTCGAGATCTTGGTGCATTTTACTGTGTGTG 683
QY 181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200

Db 684 AAAGATTCAATGACACAGCTGGCCCGGATTGCGGACAGTAAGATCATGTGTTCCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyYlIeHisSerIleLeuLysSerCys 220
Db 744 GTGAATACGGCTTTCAGGCTCTGACAGGATCATTCATCATTTTGAAGATCTCTGC 803
QY 221 IleGlnIleLeuAlaAlaGluProSerThrIleCysAlaGlyGlySerPheGlnVal 240
Db 804 ATCAAAATTCAGAGAGCTGAACCATTCACCATATGTCAGAGAGATCATTTCAAGTGTG 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db 864 GTGAGAGAAACGGCTTCCAGACATGCGGACGCTGACAGGGCTCTCTCAGCTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
Db 924 ATCAATGACTCGGTCACTCATAGAGCCCTTTCTGTGAAAGTACTTATTACTG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db 984 TGTCACGCGCTATCTTAAAGAAAGTTGGCATGAAGCTGCACCTCCAGTCAGCATGAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
Db 1044 GATGCGCTCTCTTTATCTCCAGTTCTGTATCATCATCAACACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuTrr 340
Db 1104 TCCATCTGGCCATCGCCCTGCTGATCTCTGCTCTGCTTCTTACGCTTCTCTCTG 1163
QY 341 TrrPheTrrProLeuCysCysThrValIleIleLysGluValProProProAlaGlu 360
Db 1164 TGGTTTGGCCCTCTGCTGACGTGATTCATCAAGAGGCTCCCTCACCCCTGCGGAG 1223
QY 361 GluSerLeuGlnGluAspAspAspGlyLeuProLysLysTrrProThrValAspAla 380
Db 1224 GAGAGTAGAGAAAGATGATGATGCTGCTTAAAGAAAGTGGCCAAACGCTGAGCGC 1283
QY 381 SerTyrTyrGlyGlyArgGlyValGlyYlIeLysArgMetGluValArgTrrGlyGlu 400
Db 1284 TCTTATTATGTTGGAGAGGCGTTGGAGCATTTAAAGATGAGAGTTCGTTGGGAGAA 1343
QY 401 LysGlySerThrGlnGlnGlyAlaLysLeuGlnLysAlaLysAsnAlaArgValLysMet 420
Db 1344 AAGGCTCCACAGAAAGAGGCTTAAGTTGAAAGCAAGATGCAAGGTCAAGT 1403
QY 421 ProGlnGlnGlyTyrGluPheProGluProArgAsnLeuAsnAsnMetArgPro 440
Db 1404 CCGAGCAGAGAAATGAAATTCCTGAGCCGCGAAATCTCAACAAATATGCGTGGCCT 1463
QY 441 SerSerProArgLysTrrTyrSerProIleLysGlyLysLeuAspAlaLeuTrrValLeu 460
Db 1464 TCTTCCCCCGGAAGTGTACTCTCCATCAAGGAAAACTCGATGCTTGTGGGTCTTA 1523
QY 461 LeuArgLysGlyTyrAspArgValSerValMetArgProGlnProGlyAspThrGlyArg 480
Db 1524 CTGAGAAAGATATGATCGGTGTCTGTATGCTGCACAGCAGAGACACGGGGCGC 1583
QY 481 CysIleAsnPheThrArgValLysAsnAsnGlnProAlaLysTyrProLeuAsnAsnAla 500
Db 1584 TGCAATCAACTTCACAGAGGTCAAGAACACAGCAGCCAAAGTACCACTTCACAAAGGCC 1643
QY 501 TyrHisThrSerSerProProProAlaProIleTyrThrProProProProAlaProHis 520
Db 1644 TACCACCTCTCTGCGGCTCTGCCCCCATCTACCTCCCACTCTCTGCGCCCCAC 1703
QY 521 CysProProProProProSerAlaProThrProProIleProSerProProSerThrLeu 540
Db 1704 TGCCCTCCCCCGCCCGCCAGGCGCCCTACCCCTCCATCCGCTCCACCTTCACCTT 1763
QY 541 ProProProProGlnAlaProProProAsnArgAlaProProProSerArgProProPro 560
Db 1764 CCCCCTCTCCCGCGCTCCACCTCCCAAGGCGACCTCTCTCTCCGCTCCGCTCTTCCA 1823

Db 1852 CCCACTCTCCCATCTCTCCCAACATCCACTCTCCCTCTCCAGGCCCAACC 1911
Qy 549 ProbenagalaProProProSerFarProProProaProSerVal 564
Db 1912 CTTAACAGGACCTCTCCCTCCGACCTCTCCAAAGGCTTCTGTC 1959

RESULT 5
US-09-918-715-300
; Sequence 300. Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 300
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Mouse
US-09-918-715-300

Alignment Scores:
Pred. No.: 9.01e-272 Length: 5220
Score: 2901.00 Matches: 538
Percent Similarity: 98.02% Conservative: 7
Best Local Similarity: 96.76% Mismatches: 11
Query Match: 95.90% Indels: 0
Gaps: 0

US-09-970-076-6 (1-564) x US-09-918-715-300 (1-5220)

Qy 9 LeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThrLeuValIleLeuCyAlaGlyGln 28
Db 292 CTGGGTGGGGCGCGGGGAGCTCGGGGTGACCTGGTCTGTGGCGGGAGAC 351
Qy 29 GlyIyIatGatGgIuAapGlyGlyProAlaCyStyTgIyGlyPheAapLeuTyPheIle 48
Db 352 GGGGGCCCGCGGAGATGGGGGAGCCAGCTTGCTACGAGGATTCGACCTTACTTCATC 411
Qy 49 LeuAapLySerGlySerValIleuHsiHsiTrpAangIuIeTyTyTyPheValGluGln 68
Db 412 CTGACAAAGTCAGAAAGTGTGTGTCACCACTGAAATGAATCTACTTGTGTGAGAG 471
Qy 69 LeuAlaHsiLyPheIleSerProGlnLeuAArgMetSerPheIleValPheSerThrArg 88
Db 472 TTGGTCTATGATTCATCAGCCCAAGCTTAAGAGTCTTCTCATTTGTTCTTACTGA 531
Qy 89 GlyTyThrLeuMetLyLeuThrGluAapArgGluGlnIleArgGlnGlyLeuGluGln 108
Db 532 GGGACAACTTAATCAAACTAACTGAGAGCAGGGAAACAGATCCGCAAGGCGCTGAAGAG 591
Qy 109 LeuGlnLyValIleuProGlyGlyAapThrTyTrpMetHsiGluGlyPheGluAArgAlaSer 128
Db 592 CTCGAAAGTGTCTCCAGAGAGACACTTAACATGACAGAAAGATTCGAGAGGCCCACT 651
Qy 129 GluGlnIleTyTyTyGluAapArgGlnGlyTyTrpArgThrAlaSerValIleIleAlaLeu 148
Db 652 GAGCGATTTTACTATGAAACAGTCACAGATACAGAGAGCGGAGGCTCATCTCCCTTG 711
Qy 149 ThrAapGlyGlyLeuHsiGluAapLeuPheTyTySerGlyGluArgIuAlaAapArgSer 168

Db 712 ACCGATGGGAGCTGCACGAGACCTTCTTCTACTCAGAGAGGAGGCTAACCGATCC 771
Qy 169 ArgAapLeuGlyAlaIleValTyTyCysValGlyValIyAapPheAangIuThrGlnLeu 188
Db 772 GAGACCTTGTGTGATTTGTTACTGTGGCTTGGCTGAAGATTTCAATGAACCACTGTTG 831
Qy 189 AlaArgIleAlaAapSerLyAapHsiValPheProValAapAapGlyPheGlnAlaLeu 208
Db 832 GCTCGATTCAGACAGATGAAGACCAAGTGTTCCTGTGAAACAGCGGCTTCAGGCTCTC 891
Qy 209 GlnGlyIleIleHsiSerIleLeuLyLySerCyAlaGluIleLeuAlaIleGluPro 228
Db 892 CAAGGCAATTAATCACTCAATTTTAAGAAATCTGCATTCGAATTCGGGGCTGAACCA 951
Qy 229 SerThrIleCysAlaGlyIleSerPheGlnValValValArgGlyAangIyPheAArgHsi 248
Db 952 TCCACCATCTGGCGGAGAGTCTTTCAGTGTGCTTAAGAGAAATGGCTTCCGACAT 1011
Qy 249 AlaArgAapValAapArgValIleuCySerPheLyHsiAapAapSerValThrLeuAap 268
Db 1012 GCCCGCAATGTGACAGGGTCTCTGCGACTTCAAAATCAATGACTCAGTCACGCTCAAT 1071
Qy 269 GluLyAapProPheSerValGluAapThrTyTrpLeuLeuCyAapProAlaProIleLeuGlu 288
Db 1072 GAGAGCCCTTGTGTGGAAGACATTAATTTGTGTGCCAGACCAATCTGAAAGAA 1131
Qy 289 ValGlyMetLyAaIleAlaLeuGlnValSerMetAapAapGlyLeuSerPheIleSerSer 308
Db 1132 GTTGGCATGAAGCTGCATGCAAGTTCAGATGAACACAGGCTGTCTTCTCATCTCCAGT 1191
Qy 309 SerValIleIleThrThrThrHsiCySerAapGlySerIleLeuAlaIleAlaLeuLeu 328
Db 1192 TCTGTCAATCAACACACACACTGTTACAGAGGCTCCATCTCGGAGATTTGCTCTGCTG 1251
Qy 329 IleLeuPheLeuLeuAlaLeuAlaLeuLeuTrpThrPheTrpProLeuCyCyThr 348
Db 1252 GTCTCTCTCTGTGTGCGGCTGTGGCTGTCTGTGGTGTGGCCCTCTGTGTGACA 1311
Qy 349 ValIleIleLySerGluValProProProAlaGluGluSerGluGluAapAapAap 368
Db 1312 GTGATTCATGAAGAGTCCCTCCACCCCTGTGAGAGAGTGAAGAAAGAGATGAT 1371
Qy 369 GlyLeuProLyAaLySerTrpProThrValAapAlaSerTyTyTyGlyIyArgGlyVal 388
Db 1372 GGTTCGCAAAAGAAATGGCCCAAGTAGATGCTTATTATGATGACGGGGTGTG 1431
Qy 389 GlyGlyIleLyAapMetGluValArgTrpGlyGlyLyLySerThrGluGluGlyVal 408
Db 1432 GAGGCAATTAAGAAATGAAGTCCGCTGGGAGAAAGGAGCTTCACAGAAAGGGAGCG 1491
Qy 409 LySerGluLyAaLyAaAaAlaArgValIyMetProGluGlnGluTyTyGluPhePro 428
Db 1492 AAGTTGAAGAAAGGCAAGATGCACAGTCAAGTGCACAGCAAGAAATGAGTTCCCA 1551
Qy 429 GluProArgAapLeuAapAaAaAaMetAArgArgProSerSerProArgLySerTySer 448
Db 1552 GAACCCCGAAACCTCAACACACATGCGCGGCTTCTCTGCGTCCGAAAGTGGTACTCG 1611
Qy 449 ProIleLySerLyLySerAapAlaLeuTrpValIleLeuAArgLyGlyTyTyAapArgVal 468
Db 1612 CCATCAAGGAGAAACCTCGATGCTTGTGGGTCTGTGAGAAAGAAATGACCGGAGTG 1671
Qy 469 SerValMetArgProGlnProGlyAapThrGlyAArgCyAlaAapPheThrArgValIy 488
Db 1672 TCTGTGTAGGCGCACAGCGAGAGACCGGAGCGCTGTATCACTTACACAGGTGAAG 1731
Qy 489 AapAapGlnProAlaLyTyTyProLeuAapAaAaIaTyTrpHsiThrSerSerProProPro 508
Db 1732 AACAGTACGACGACGAAATATCCCTGGAACAACACCTAACACCCAGCTCCCACTCCC 1791
Qy 509 AlaProIleTyTyTrpProProProProAlaProHsiCyAapProProProProSerAla 528
Db 1792 GCTCTTATTAACACACCCCACTGCTCCCACTGCTCCCACTGCTCCCACTGCTCCCACTG 1851

QY 529 ProthrrProrolleProserProserThrieuProProProGlnAlaProPro 548
 DB 1852 CCCACTCCCTCCCACTTCCTCCCACTCATCTCCCTCCCTCCCAAGGCCCAACC 1911

QY 549 ProAsnArgAlaProProProProserArgProProProArgProSerVal 564
 DB 1912 CCTAACAGGCACTCCCTCCCTCCCACTCCCTCCCAAGGCCCTTCTC 1959

RESULT 6
 US-10-302-172-250
 Sequence 250, Application US/10302172
 Publication No.: US20040053250A1
 GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
 APPLICANT: Xue, Aidong J.
 APPLICANT: Drmanac, Radolje T.
 TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids and
 FILE REFERENCE: 803.1CNCp
 CURRENT APPLICATION NUMBER: US/10/302,172
 CURRENT FILING DATE: 2002-11-21
 PRIOR APPLICATION NUMBER: US 10/225,251
 PRIOR FILING DATE: 2002-08-20
 PRIOR APPLICATION NUMBER: PCT US02/05095
 PRIOR FILING DATE: 2002-03-05
 PRIOR APPLICATION NUMBER: US 09/799,451
 NUMBER OF SEQ ID NOS: 950
 SOFTWARE: pc FL_genes Version 2.0
 SEQ ID NO 250
 LENGTH: 3981
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (297) ..(1118)
 US-10-302-172-250

Alignment Scores:
 Pred. No.: 2,5e-186 Length: 3981
 Score: 2022.00 Matches: 372
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 66.84% Mismatches: 0
 Query Match: 13 Indels: 0
 DB: 13 Gaps: 0

US-09-970-076-6 (1-564) x US-10-302-172-250 (1-3981)

QY 193 AppSerLyAspHisValaPheProValaAsnAspGlyPheGlnAlaLeuGlnGlyIleIle 212
 DB 3 GACAGTAGAGATCATGTGTGTTCCCGTAGATGACGGCTTTCGAGGCAATGATC 62

QY 213 HisSerIleLeuLybAspSerCysIleGluIleLeuAlaGluProSerThrIleCys 232
 DB 63 CACTCAATTTTGAAGAGTCCCTGCATCGAAATTTCTAGCGCTGACCAATCCACATATAT 122

QY 233 AlaGlyGluSerPheGlnValaValaArgGlyAsnGlyPheArgHisAlaArgAsnVal 252
 DB 123 GCAGGAGATCATTTTCAGTGTGCTGAGAGGAAACGGCTTCGACATGCCGCAACGTG 182

QY 253 AspArgValaLeuCysSerPheGlyIleAsnAspSerValThrLeuAsnGluysProPhe 272
 DB 183 GACAGGCTCTCTGACGCTTCAGATCATGACTCGGTCACTCAATAGAGAGCCCTTT 242

QY 273 SerValGluAspThrTyrlleuLeuCysProAlaProIleLeuLyGluValGlyMetLys 292
 DB 243 TCTGTGAAGATCATTTTACTGTGTCCAGGCCCTTATCTTAAAGAAAGTTGGCATGAA 302

QY 293 AlaAlaLeuGlnValaSerMetAsnAspGlyLeuSerPheIleSerSerValIleIle 312
 DB 303 GCTGCACTCCAGGTCAGCATGAACGATGGCCTCTCTTTATCTCCAGTTCTGTCAATC 362

QY 313 ThrThrHisCysSerAspGlySerIleLeuAlaIleAlaLeuIleLeuPheLeu 332
 DB 363 ACCACACACACTGTTCATGACGTTCCATCCCGGCATCGCCCTCTATCTGTTCCTG 422

QY 333 LeuLeuAlaLeuAlaLeuLeuTrpPheTrpProLeuCysCysThrValIleIleLys 352
 DB 423 CTCCTAGCCCTGCTCTCTCTGTGTGTGCTGACCCCTCTGCTGCATGTGATATCAAG 482

QY 353 GluValaProProProProAlaGluGluSerGluGluGluAspAspGlyLeuProLys 372
 DB 483 GAGGTCCTCCACCCCTGCGCAGAGAGTAGAGAAAGATGATGATGTGCTGCTAAG 542

QY 373 LysLysTrpProThrValaAspAlaSerTyrlGlyGlyValaGlyValaGlyLys 392
 DB 543 AAAAGTGCCCAACGCTAGACCTCTTATTTATGTGGAGAGGCGCTTGAGGCAATTAA 602

QY 393 ArgMetGluValaArgTrpGlyGlyLysGlySerThrGluGluGlyAlaLysLeuGlyLys 412
 DB 603 AGAATGAGAGTTCGTTGGGAGAAAGAGGCTCCACAGAAAGAGTGAATTGGAAGAA 662

QY 413 AlaLysAsnAlaArgValaLysMetProGluGlnGluTyrlGluPheProGluProArgan 432
 DB 663 GCMAAGAAATGCAAGAGTCAGAGTCCGAGCAGAGAAATGATATTCCTGAGCGGAAT 722

QY 433 LeuAsnAsnAsnMetArgArgProSerSerProArgLysTrpTyrlSerProIleLysGly 452
 DB 723 CTCACACACATATATCGTCGCTCTTCTCCCGGAAAGTGTACTCTTCATCAAGGA 782

QY 453 LysLeuAspAlaLeuTrpValaLeuLeuArgLysGlyTyrlAspArgValaSerValMetArg 472
 DB 783 AAATCGATGCTTGTGGGTCTTACTGAGAAAGATATGATCGTGTCTGTATGCGT 842

QY 473 ProGlnProGlyAspThrGlyArgGlyIleAsnPheThrArgValaLysAsnGlnPro 492
 DB 843 CCACAGCAGAGAGACGGGGCGTCGATCACTTCACACAGGTCAGAAACACAGCA 902

QY 493 AlaLysTyrlProLeuAsnAsnAlaTyrlHisThrSerSerProProProAlaProIleTyrl 512
 DB 903 GCCAGTACCCACTCAACAGCGCTTACACACTCTCTGCGGCTCTGCCCCCATCTAC 962

QY 513 ThrProProProProAlaProHisCysProProProProProProSerAlaProThrProPro 532
 DB 963 ACTCCCCCACTCTGACACCCCACTGCGCTCCCGCCGCCGCCCAAGCCCTACCTCC 1022

QY 533 IleProSerProProSerThrIleuProProProProGlnAlaProProProAsnArgAla 552
 DB 1023 ATCCGTCCTCCCACTTCCACCTTCCCTCTCCCAAGGCTCCACCTCCCAAGGGCA 1082

QY 553 ProProProSerArgProProProArgProSerVal 564
 DB 1083 CCTCCTCCTCCGCGCTCTCTCAAGGCTTGTGTC 1118

RESULT 7
 US-09-796-753-23
 Sequence 23, Application US/09796753
 Publication No.: US20030027998A1
 GENERAL INFORMATION:
 APPLICANT: McCarthy, Sean A.
 TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 FILE REFERENCE: 7853-227-999
 CURRENT APPLICATION NUMBER: US/09/796,753
 CURRENT FILING DATE: 2001-03-01
 PRIOR APPLICATION NUMBER: 09/183,175
 PRIOR FILING DATE: 1998-10-30
 PRIOR APPLICATION NUMBER: 09/223,094
 PRIOR FILING DATE: 1998-12-30
 PRIOR APPLICATION NUMBER: 09/223,546
 PRIOR FILING DATE: 1998-12-30
 PRIOR APPLICATION NUMBER: 09/224,246
 PRIOR FILING DATE: 1998-12-30
 PRIOR APPLICATION NUMBER: 09/259,388
 PRIOR FILING DATE: 1999-02-26
 PRIOR APPLICATION NUMBER: 60/122,458

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/ PRIOR FILING DATE: 1999-03-01
/ PRIOR APPLICATION NUMBER: 09/312,359
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: 09/336,536
/ PRIOR FILING DATE: 1999-06-18
/ PRIOR APPLICATION NUMBER: 09/342,687
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 09/345,464
/ PRIOR FILING DATE: 1999-06-30
/ PRIOR APPLICATION NUMBER: 09/365,164
/ PRIOR FILING DATE: 1999-07-30
/ PRIOR APPLICATION NUMBER: 09/399,723
/ PRIOR FILING DATE: 1999-09-20
/ PRIOR APPLICATION NUMBER: 09/409,634
/ PRIOR FILING DATE: 1999-09-30
/ PRIOR APPLICATION NUMBER: 09/471,179
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 09/474,071
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/474,072
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/514,010
/ PRIOR FILING DATE: 2000-02-25
/ PRIOR APPLICATION NUMBER: 09/516,745
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: 09/572,002
/ PRIOR FILING DATE: 2000-05-14
/ PRIOR APPLICATION NUMBER: 09/597,993
/ PRIOR FILING DATE: 2000-06-19
/ PRIOR APPLICATION NUMBER: 09/599,596
/ PRIOR FILING DATE: 2000-06-22
/ PRIOR APPLICATION NUMBER: 09/630,334
/ PRIOR FILING DATE: 2000-07-31
/ PRIOR APPLICATION NUMBER: 09/606,565
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: 09/606,317
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: 09/665,666
/ PRIOR FILING DATE: 2000-09-20
/ PRIOR APPLICATION NUMBER: 09/677,751
/ PRIOR FILING DATE: 2000-09-30
/ NUMBER OF SEQ ID NOS: 162
/ SEQ ID NO 23
/ LENGTH: 4417
/ TYPE: DNA
/ ORGANISM: Mouse
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3)...(1145)
US-09-796-753-23

Alignment Scores:
Pred. No.: 8,886-186 Length: 4417
Score: 2017.00 Matches: 371
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 98.15% Mismatches: 4
Query Match: 66.68% Indels: 0
DB: 10 Gaps: 0

US-09-970-076-6 (1-564) x US-09-796-753-23 (1-4417)
QY 187 GlnLeuAlaArgIleAlaAspSerLyAspHisValPheProValAsnAspGlyPheGln 206
DB 12 CAGTTGGCTCGGATTGCAGACAGTAAGACCAAGTGTTCCTGTGAAGAGCGGCTTCAG 71
QY 207 AlaLeuGlnGlyIleIleHisSerIleLeuLylySerCysIleGluIleuAla 226
DB 72 GCTCTCCAGAGCATATCCATCAATTTAAAGAAATCCTGCATCGAAATTCGGCGGCT 131
QY 227 GluProSerThrIleCysAlaGlyGlySerPheGlnValValArgGlyAsnGlyPhe 246
DB 132 GAACATCCACCATCTGCGGGAAGGTCCTTCAAGTGTCGTAAGAGAAATGGCTTC 191
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QY 247 ArgHisAlaArgAsnValAspArgValLeuCysSerPheLyIleAsnAspSerValThr 266
DB 192 CGACATGCCCGCATGTGACAGGGCTCCTGACAGTTCAAAATCATATGACTGATCAGC 251
QY 267 LeuAsnGlySerProPheSerValGluAspThrTyrtleuLeuCysProAlaProIleLeu 286
DB 252 CTCAATAGAAAGCCCTTGTGCGGAAGACATTAATTTGCTGTGCCAGCACCAATCTTG 311
QY 287 LyseGluValGlyMetCysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIle 306
DB 312 AAAGAAGTTGGCATGAAGAGCTGCAGCTGCAGTCAGATGAAGACGGCTCTCTTCA 371
QY 307 SerSerSerValIleIleThrThrThiCysSerAspGlySerIleLeuAlaIleAla 326
DB 372 TCAGTTCTGTGCATCATCACCAACACACTGTTCAAGCGGCTCCATCTCGGCGATGGCT 431
QY 327 LeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTPTTPPheTTPProLeuCys 346
DB 432 CTGCTGTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
QY 347 CysThrValIleIleIleLyseGluValProProProProAlaGluSerGluGluAsp 366
DB 492 TGCAAGATGATCATCAAGAGAGTCCCTCCACCCCTGTGAGAGAGTGAAGAAAGAC 551
QY 367 AspAspGlyLeuProLylyLylyeTTPProThrValAspAlaSerTyTyGlyGlyArg 386
DB 552 GATGATGGTTTGCAGAAAGAAATGAGCCCACTAGATGCTCTTATGAGTGAGCGC 611
QY 387 GlyValGlyGlyIleLyseArgMetGluValArgTTPGlyGlySerThrGluGlu 406
DB 612 GGTGTGGAGCATTAAGAAATGAGAGTCCGCGGAGAAAGGCTCCACAGAAAGAA 671
QY 407 GlyAlaLyseGluGlyValAlaLyseAsnAlaArgValLyseMetProGluGlnGly 426
DB 672 GGGCGCAAGTTAGAAAGAGCAAGATGACAGATCAAGATCCAGAGCAAGATATAG 731
QY 427 PheProGluProArgAsnLeuAsnAsnMetArgArgProSerSerProArgLyseTTP 446
DB 732 TTCCAGAAAGCCCGAAACCTCAACAAACATGCGCGGCTCTCTGCTCGGAAGTGG 791
QY 447 TyrtSerProIleLyseGlyLylyLeuAspAlaLeuTTPValLeuAlaGlyLyse 466
DB 792 TACTGCGCCATCAAGGAGAACTGATGCTGTGTGCTGTGAGAAAGATATGAC 851
QY 467 ArgValSerValMetCysProGluInProGlyAspThrGlyArgCysIleAsnPheThrArg 486
DB 852 CGAGTGTCTGTGAAGAGCCACACAGAGACAGCGGAGCCCTGTATCAATTCACAG 911
QY 487 ValLyseAsnAsnGlnProAlaLyseTyrtProLeuAsnAsnAlaTyrtHisSerSerPro 506
DB 912 GTGAAGAAAGATGACAGCCAGCAAGTATCCCTGAAACACCTACACCCAGCTCCCA 971
QY 507 ProProAlaProIleTyrtThrProProProProAlaProHisCysProProProPro 526
DB 972 CTTCCCGCTCTATCTACACACCCCAACCCCTCTCCCACTCCCTCCCAAGCCCCC 1031
QY 527 SerAlaProThrProProIleProSerProProSerThrLeuProProProGluAla 546
DB 1032 AGTGCCCACTCTCTCCATCTCTCCCAACATCACTCTCCCTCCCTCTCTCAAGGCC 1091
QY 547 ProProProAsnAlaAlaProProProProSerArgProProProArgProSerVal 564
DB 1092 CCACCCCTTAACAGGAGCACTCCCTCCGAGCTCTCCAAAGGCTTGTGTC 1145

RESULT 8
US-10-038-307-3
; Sequence 3, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYINAK
; APPLICANT: Judith J. HEALEY
```

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; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows, Version 4.0
; SEQ ID NO 3
; LENGTH: 4417
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(1145)
US-10-038-307-3

Alignment Scores:
Pred. No.: 8,886-186 Length: 4417
Score: 2017.00 Matches: 371
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 98.15% Mismatches: 4
Query Match: 66.68% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-6 (1-564) x US-10-038-307-3 (1-4417)
QY 187 GlnLeuAlaArgIleAlaAspSerIleValPheProValAsnAspGlyPheGln 206
DB 12 CAGTGGCTCGGATTGACAGACAGTAAGACCGTGTTCCTGTAACACCGCTTCCAG 71
QY 207 AlaLeuGlnGlyIleIleHisSerIleLeuValSerCybIleGlnIleLeuAla 226
DB 72 GCTCTCCAAAGCATATTCACCTCAATTTAAAGAAATCTGCATGAAATTTGGCGCT 131
QY 227 GluProSerThrIleCysAlaGlySerPheGlnValValArgGlyAsnGlyPhe 246
DB 132 GAACCATCCACCATCTGCGCGGAGAGTCTTTCAAGTGTGTAAAGAGAAATGGCTTC 191
QY 247 ArgHisAlaArgAsnValAspArgValLeuCysSerPheValIleAsnAspSerValThr 266
DB 192 CCACATGCCCCGAAAGTGACAGGGCTCTTCAGCTTCAAAATCAATGACTCAGTCACG 251
QY 267 LeuAsnGluValProPheSerValGluAspThrTyrLeuLeuCybProAlaProIleLeu 286
DB 252 CTCATATGAAACCCCTTCTGCTGGAAGACATTTATTTGCTGTGCCAGCAATCTTG 311
QY 287 LysGluValGlyMetIleValAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIle 306
DB 312 AAAGAAGTTGGCATGAAGCTGACAGTCAGATGAAACGACGGCTGTCTTCATC 371
QY 307 SerSerSerValIleIleThrThrThrHisCysSerAspGlySerIleLeuAlaIleAla 326
DB 372 TCACATTTCTGATCATCTACACCACTCTTCAGAGGGCTCCATCTTGCAGATTGCT 431
QY 327 LeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyrPheThrProLeuCyb 346
DB 432 CTGCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
QY 347 CysThrValIleIleIleValIleProProProAlaGluGluSerGluGluAsp 366
DB 492 TCACAGTATCATCATCAAGAGGTCCTCCACCCCTGTTGAGAGAGTGAAGAAAGAC 551
QY 367 AspAspGlyLeuProIleValSerValPheProThrValAspAlaSerTyrTyrGlyValArg 386
DB 552 GATGATGTTTCCAAAGAAAGAAAGTGGCCACAGTAGATGCTTATATATGATGACCC 611
QY 387 GlyValGlyGlyIleValSerMetGluValArgTyrGlyGlySerThrGluGln 406
DB 612 GGTGTGGAGGCAATTAAGAAATGAGTCCGCTGGGAGAAAGGGCTCCACAGAAAG 671
QY 407 GlyAlaValLeuGluValValAlaValAsnAlaArgValValSerProGluGlnIleTyrGln 426
DB 672 GGGGCGAAGTTAGAAAGCAAGAAAGATGACAGATCAAGATGTCAGAGCAAGAAATATGAG 731

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QY 427 PheProGluProArgAsnLeuAsnAsnMetArgArgProSerSerProArgIleTyr 446
DB 732 TTCCAGAAACCCGAAACCTCAACAACAATGGCGGGCTTCTGCTCGGAAGTGG 791
QY 447 TyrSerProIleValGlyValLeuAspAlaLeuThrValIleLeuArgGlyTyrAsp 466
DB 792 TACTGCCCCATCAAGGGAACCTCGATCCCTGTGGGTTCGTGAGAAAGATATGAC 851
QY 467 ArgValSerValMetArgProGlnProGlyAspThrGlyValArgCysIleAsnPheThrArg 486
DB 852 CGAGTGTGTGAGAGCCACAGCAGAGACAGCGGACCTGTATATCACTTCAACCA 911
QY 487 ValIleAsnAsnGlnProAlaValSerTyrProLeuAsnAsnAlaTyrHisThrSerSerPro 506
DB 912 GTGAAGAACACTGACCGCCAGCAAGATCCCTGAACAAACACTTCAACCCAGCTCCCA 971
QY 507 ProProAlaProIleTyrThrProProProProAlaProHisCysProProProPro 526
DB 972 CCTCCGCTCTCTATCTACACACCCCACTCCCTGCTCCCACTGCTCCCAAGGCC 1031
QY 527 SerIleProThrProProIleProSerProProSerThrLeuProProProGlnAla 546
DB 1032 AGTGCCTCCACTCTCCCATTCCTTCCACCATTCACCTTCCCTCTCTCTGAGGC 1091
QY 547 ProProProAsnArgAlaProProProSerArgProProArgProSerVal 564
DB 1092 CCACCCCTTAACAGGACCTTCCCTCCGACCTCTCCAGGCTTCTGTG 1145

RESULT 9
US-10-201-292-3
; Sequence 3, Application No. 10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4417
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(1145)
US-10-201-292-3

Alignment Scores:
Pred. No.: 8,886-186 Length: 4417
Score: 2017.00 Matches: 371
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 98.15% Mismatches: 4
Query Match: 66.68% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-6 (1-564) x US-10-201-292-3 (1-4417)
QY 187 GlnLeuAlaArgIleAlaAspSerIleValPheProValAsnAspGlyPheGln 206
DB 12 CAGTGGCTCGGATTGACAGACAGTAAGACCGTGTTCCTGTAACACCGCTTCCAG 71
QY 207 AlaLeuGlnGlyIleIleHisSerIleLeuValSerCybIleGlnIleLeuAla 226
DB 72 GCTCTCCAAAGCATATTCACCTCAATTTAAAGAAATCTGCATGAAATTTGGCGCT 131
QY 227 GluProSerThrIleCysAlaGlySerPheGlnValValArgGlyAsnGlyPhe 246
DB 132 GAACCATCCACCATCTGCGCGGAGAGTCTTTCAAGTGTGTAAAGAGAAATGGCTTC 191

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QY 241 ValArgGlyAenGlyPheArgHisAlaArgAenValAspArgValLeuCySerPheLeu 260
DB 864 GTGAGAGAAACGGCTTCCGACATGCCCCGCAACGTGACAGGGTCTCTGCAAGCTTCAAG 923
QY 261 TLeaAenAspSerValThrLeuAenGlyUlyPProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACTCGGTCACTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACACTTATTACTG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetLeu 300
DB 984 TGTCCAGCGCCCTATCTTAAAGAGTTGGCATGAAAGCTGCACTCAGTCCAGTCCAGTGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThiCysSerAspGly 320
DB 1044 GATGCGCTCTCTTTTATCTCCAGTTCTGCTCATCATCACCAACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyr 340
DB 1104 TCCATCTGGCCATGCGCCCTGCTGATCCTGTTCTGCTCCTGAGCCCTGCTCTG 1163
QY 341 TrpPheTyrProLeuCySerThrValIleIleLysGluValProProProAlaGlu 360
DB 1164 TGGTTCGGCCCTCTGCTGCACTGATTAACAAGAGTCCCTCCACCCCTGCGAG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAGAA 1235
RESULT 11
US-10-159-563-58
; Sequence 58, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TREATING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-58
Alignment Scores:
Pred. No.: 1,78e-174 Length: 1454
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.61% Indels: 0
DB: 16 Gaps: 0
US-09-970-076-6 (1-564) x US-10-159-563-58 (1-1454)

QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
DB 324 GAATCTTATCTTTGTGGAACAGTTGGCTACAAATTCATCAGCCCACTTGAGATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
DB 384 TCTTTATTTGTTTCTCCACCGAGAAACAACCTTAATGAACCTGACAGAAACAGAGAA 443
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
DB 444 CAATCCCTCAAGCCTTGAAGAACTCCAGAAAGTTCGCCAGAGAGAGACACTTAACATG 503
QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAspArgGlnGlyTyrArg 140
DB 504 CATGAAGATTGAAAGGGCCAGTGAAGCATTTTATTTGAAACAGCAAGGGTACAGG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheThr 160
DB 564 AAGCCACGTCATCATTTGCTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 623
QY 161 SerGluArgGluAlaAspArgSerThrArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTAATAGGCTTCGAGATCTTGATGCAATGTTTACTGTTGGTGTG 683
QY 181 LysAspPheAenGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAAGATTCAATGAGACACAGCTGGCCGGAATGGGACAGTAAAGATCATGTTTCCC 743
QY 201 ValAenAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
DB 744 GTGAATGACGGCTTCAAGGCTCTGCAAGGCAATCATCCACTCAATTTTGAAGAGTCCG 803
QY 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
DB 804 ATCGAATCTTACGAGCTGAACCATCCACATATGTGACAGAGAGTCAATTCAGATTGTC 863
QY 241 ValArgGlyAenGlyPheArgHisAlaArgAenValAspArgValLeuCySerPheLeu 260
DB 864 GTGAGAGAAACGGCTTCCGACATGCCCCGCAACGTGACAGGGTCTCTGCAAGCTTCAAG 923
QY 261 TLeaAenAspSerValThrLeuAenGlyUlyPProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACTCGGTCACTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACACTTATTACTG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetLeu 300
DB 984 TGTCCAGCGCCCTATCTTAAAGAGTTGGCATGAAAGCTGCACTCCAGTCCAGTGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThiCysSerAspGly 320
DB 1044 GATGCGCTCTCTTTTATCTCCAGTTCTGCTCATCATCACCAACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyr 340
DB 1104 TCCATCTGGCCATGCGCCCTGCTGATCCTGTTCTGCTCCTGAGCCCTGCTCTG 1163
QY 341 TrpPheTyrProLeuCySerThrValIleIleLysGluValProProProAlaGlu 360
DB 1164 TGGTTCGGCCCTCTGCTGCACTGATTAACAAGAGTCCCTCCACCCCTGCGAG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAGAA 1235
RESULT 12
US-10-038-307-17
; Sequence 17, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTHMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OKAYMAK


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; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-201-292-17

Alignment Scores:
Pred. No.: 1,076-151 Length: 1674
Score: 1661.00 Matches: 361
Percent Similarity: 67.54% Conservative: 26
Best Local Similarity: 63.00% Mismatches: 81
Query Match: 54.91% Indels: 107
DB: 15 Gaps: 12

US-09-970-076-6 (1-564) x US-10-201-292-17 (1-1674)
QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 13 ATGGCCACGGCGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 72
QY 21 LeuValIleuIleCysAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTrp 40
DB 73 CTGGTGCTCATCTGCGCCGGGCAAGGGGACGAGGAGAGATGGGGGTCCAGCTGCTAC 132
QY 41 GlyGlyPheAspLeuTrpThrIleLeuAspGlySerGlySerValIleuHisStrpAen 60
DB 133 GCGGAGTTTGACCTGATCTCACTTTTGACCAATCAGAAAGTGCTGTCACCACTGGAA 192
QY 61 GluIleTrpTrpPheValGluGlnLeuAlaHisIleValPheIleSerProGlnLeuArgMet 80
DB 199 GAAATCTATTACTTGTGGAAAGCTTGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 252
QY 81 SerPheIleValPheSerThrArgGlyThrTrpLeuMetIleLeuThrGluAspArgGlu 100
DB 253 TCCTTATTGTTTCCACCCGAGGAAACACCTTAATGAACTGACAGAGACAGAGA 312
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnIleValLeuProGlyGlyAspThrTrpMet 120
DB 313 CAAATCCGTCAGAGGCTTAGAGAACTCCAGAAAGTTCTCCAGAGGAGACACTTAACATG 372
QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTrpTrpGluAspArgGlnIleTrpArg 140
DB 373 CATGAAGGATTTGAAAGGCGCAGTGGCAAGTTTATTATGAAACAGACAGAGGATACAG 432
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGlyAspLeuPheTrp 160
DB 433 ACAGCAGAGGTATCATCTTCTTGACTGATGAGAACTCATGAGAAATCTCTTTTCTAT 492
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValIleCysValGlyVal 180
DB 493 TCAGAGAGGAGGAGCTAATAGCTCTCGAGACTTGGGCAATGTTTAACTGTTGGTGG 552
QY 181 LysAspPheAsnGlnTrpGlnIleuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 553 AAAGATTTTAAATGAGACACAGCTGGCCCGAATTGGCGACAGTAAGGATATGTGTTCC 612
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
DB 613 GTGAATGACGGCTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAAGCTCTCC 672
QY 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
DB 673 ATCGAAATCTTAGCAGCTCAACATCCACCATATATGCGAGGAGATCATTTTAAAGTTGTC 732
QY 241 ValArgGlyLysGlnGlyPheArgHisAlaIleAsnValAspArgValLeuCysSerPheLys 260

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DB 723 GTGAGAGGAACGGCTTCAGACATCCCGCAACGTGACAGGGTCTCTGACGTTCAAG 792
QY 261 IleAsnAspSerValThrLeuAsnGlyLysProPheSerValGluAspThrTrpLeuLeu 280
DB 793 ATCAATGATCTCGGTACACTCAATGAGAACCCCTTTCTGGAGAGATTAATTAATCTG 852
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaIleLeuGlnValSerMetAsn 300
DB 853 TGTCCAGGCGCTATTTAAAGAGTGTGCATGAAGCTGACCTCAGGTGACATGAGAAC 912
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrTrpHisCysSerAspGly 320
DB 913 GATGCGCTCTCTTTATCTCAGTTCTGTATCATACACACACACTGTTCTACCGT 972
QY 321 -----SerIleLeuAla 324
DB 973 CCCAATCTTCTGACAAACTCACACATGCCAGCTGCCAGACACTGAACTCCGGAGG 1032
QY 325 IleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrpTrpPheTrpPro 344
DB 1033 GCACCGTCAAGTCTCTCTTC----- 1053
QY 345 LeuCysCysThrValIleIleLeuGluValProProProAlaGlu----- 360
DB 1054 -----CCCCAAGAACCAAGAGACACCTCATGATC 1083
QY 361 -----GluSerGluGluAspAspGly 369
DB 1084 TCCCGGACCCCTGAGGTCAATGCGGTGGTGAGCGAGCAGACAGAGAC----- 1134
QY 370 LeuProLysLysTrpProThrValAspAlaSerTrpTrpGlyGlyArg----- 386
DB 1135 -----CTGAGGTCAAGTTCAACTGTGACGT-GAGCGGGTGAAGGT 1175
QY 387 -----GlyValGlyIleLysValArgMetGluValArgTrpGlyGlu 400
DB 1176 GCATTAATGCCAAGAACCCCGGAGAGAGACAGTACAAACAGCACTACCGTGTGTGAG 1235
QY 401 Lys-----GlySerThrGlu-----GluGlyAlaLysLeuGlnLysAla 413
DB 1236 GGTCTTCACCGTCTGACACAGAGTGGCTGGAATGCAAGAGTCAAGTCAAGTCTC 1295
QY 414 LysAsnAlaArgValLysMetProGluGlnGlyTrpGluPheProGluProArgAsnLeu 433
DB 1296 CAACAACCC---CTCCAGCCCTCATGAGAAACCATCT-CCAAAGCCAAAGGGCAGC 1351
QY 434 AsnAsnAsnMetArgArgProSerSerProArgLysTrpTrpTrpSer---ProIleLysGly 452
DB 1352 CCCGGAACACACAGGTGTACACCTGCCCCATCCCGGAGTGAAGCTGACCAAGAACAG 1411
QY 453 LysLeuAspAlaLeuTrpValLeuLeuArgLysGlyTrpAspArgValSerValMetArg 472
DB 1412 TCAGCTGACCTGCTGCTG-----TCAAAGCTTCTATCCACAGC 1450
QY 473 ProGlnProGlyAspThrGlyArgCysIleAsnPheThrArgValLysAsnAsnGlnPro 492
DB 1451 ACATGCGCGTGG---AGTGGAGAGCAATGGGACCGCAGAG----- 1489
QY 493 AlaLysTrpProLeuAsnAsnAlaLysHisIleThrSerSerProProAlaProIleTrp 512
DB 1490 -----ACAACTTCAAGACCAACCGCTCCCGTGGTGG 1519
QY 513 ThrProProProAlaProHisCysArgProProProPro 525
DB 1520 ACTCGGACGGCTCTTCTTCTCTACAGCAAGCTCACC 1558

RESULT 14
US-10-038-307-15
; Sequence 15, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTHMAN

```

APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKANAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038.307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1650
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-15

Alignment Scores:

Pred. No.:	7,066-151	Length:	1650
Score:	1652.50	Matches:	361
Percent Similarity:	67.78%	Conservative:	26
Best Local Similarity:	63.22%	Mismatches:	81
Query Match:	54.63%	Indels:	105
		Gaps:	12

US-09-970-076-6 (1-564) x US-10-038-307-15 (1-1650)

Qy 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db 1 ATGGCCAGGGCGAGAGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGCCCACT 60
Qy 21 LeuValLeuIleCysAlaGlyGlnGlyIleArgArgGluAspGlyGlyProAlaCysArg 40
Db 21 CTGGGCTCATCTGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Qy 41 GlyGlyPheAspLeuTrpPheIleuAspLysSerGlySerValLeuAlaHisTrpAsn 60
Db 41 GGGGATTTGACCTGACTCTTCTTTGGACAAATAGAGAGGAGGAGGAGGAGGAGGAGGAGG 180
Qy 61 GluIleTrpPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
Db 61 GAATCTATTACTTGTGGACAGTGGCTCCAAATTCATCAGCCCAAGTTGAGATG 240
Qy 81 SerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArgGlu 100
Db 81 TCCCTTATTGTTTCTCCACCGGAGAACTTAATGAACTGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 101 GlnIleArgGlnGlyLeuGlnGlnLeuGlnLysValLysProGlyGlyAspThrTrpMet 120
Db 101 CAAATCCGTCAGAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGGAGAGAGAGAGAGAGAG 360
Qy 121 HisGlnGlyPheGluArgAlaSerGlnGlnIleTrpTrpGluAsnArgGlnGlyTrpArg 140
Db 121 CATGAGAGATTTGAAAGGGCCAGTGAAGCATTTATTGAAAACAGCAAGGGATCAGG 420
Qy 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAspLeuPhePheTrp 160
Db 141 ACAGCCACGCTCATATGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 480
Qy 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTrpCysValAlaGlyVal 180
Db 161 TCAGAGAGAGAGGCTTAATGAGTCTGAGATCTTGGTGAATTTGTTACTGTTGGTGTG 540
Qy 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db 181 AAAAGTTTCATGAGACACAGCTGCCCGGATGGCGACAGTAAAGATCATGTGTTTCC 600
Qy 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
Db 201 GTGAATGACGCGCTTCAAGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGCTCGC 660
Qy 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGlyLysPheGlnValAla 240
Db 221 ATCGAAATTTTAGCAGCTGAACCATCCACCATATGTGAGAGAGAGTCAATTCAGATTGTC 720

Qy 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValaAspArgValLeuCysSerPheLys 260
Db 721 GTGAGAGAAACGGCTTCCGACATGCCCGCAAGCTGAGAGGGTCTCTGAGCTTCAAG 780
Qy 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTrpLeuLeu 280
Db 781 ATCATGACTCGGCACATCAATGAGAAAGCCCTTCTGTGAAAGTACTTATTATTCG 840
Qy 281 CysProAlaProIleLeuLysGluValAlaGlyMetLysAlaAlaLeuGlnValaSerMetAsn 300
Db 841 TGTCCAGCGCTTATCTTAAGAGATTGGCATGAAGCTGCACTCCAGGTACATGAC 900
Qy 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
Db 901 GATGCGCTCTCTTTATCTTCAGATTCTGTATCATATCAACACACACTGTTTCCCAA 960
Qy 321 Ser----- 326
Db 961 TCTTCTGACAAACTCACATGCCACCGTCCACACCTGAACCTCTGGGGGAGCCG 1020
Qy 327 LeuLeuIleuPheLeuLeuLeuAlaLeuAlaLeuLeuTrpTrpPheTrpProLeuCys 346
Db 1021 TCAGCTTCTCTTC----- 1035
Qy 347 CysThrValIleIleLysGluValProProProProAlaGlu----- 360
Db 1036 -----CCCCAAACCCAAAGGACACCTCATGATCTCCCG 1071
Qy 361 -----GluSerGlnGlnGluAspAspGlyLeuPro 371
Db 1072 ACCCGTAGGTCAATCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1116
Qy 372 LysLysLysTrpProThrValaAspLysTrpTrpGlyIleArg----- 386
Db 1117 -----CTGAGGTCAAGTTCAACTGATGCT- GAGCGCGCTGAGGTGCAATA 1153
Qy 387 -----GlyValGlyGlyIleLysArgMetGluValArgTrpGlyGlyLys--- 401
Db 1164 TGCCAGACAAAGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1223
Qy 402 -----GlySerThrGlu---GluGlyAlaLysLeuGlnLysAlaLysAsn 415
Db 1224 CACCGTCTGCACCAAGGACTGCTGATGAGCAAGAGTAAAGGACAGTCTTCAACAA 1283
Qy 416 AlaArgValLysMetProGlnGlnGlyTrpGluPheProGluProAlaGlnLeuAsnAsn 435
Db 1284 AGC---CCTCCACGCCCCCATCGAATAACCATCT-CCAAAGCCAAAGGCGACGCCGAG 1339
Qy 436 AsnMetArgArgProSerSerProArgLysTrpTrpSer---ProIleLysGlyLysLeu 454
Db 1340 AACCAAGAGGTACACCCCTGCCCATCCCGGATGAGTGAACCAAGAACAGGTCAAGCC 1399
Qy 455 AspAlaLeuTrpValLeuLeuArgLysGlyTrpAspArgValSerValMetArgProGln 474
Db 1400 TGACCTGCTG-----TCAAGGCTTCTATCCAGGACGACATCG 1438
Qy 475 ProGlyAspThrArgCysIleAsnPheThrArgValLysAsnAsnGlnProAlaLys 494
Db 1439 CCGTGG---AGTGGAGAGCAATGGCGACCGGAGA----- 1471
Qy 495 TyrProLeuAsnAsnAlaTrpHisThrSerSerProProAlaProIleTrpThrPro 514
Db 1472 -----ACAACTAAAGACACAGCGCTCCGCTGAGATCTCG 1507
Qy 515 ProProProAlaProHisCysProProProPro 525
Db 1508 ACGGCTCTTCTTCTCTTCAAGCAAGCTCAAG 1540

RESULT 15

US-10-201-292-15
; Sequence 15, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:44:26 ; Search time 33.2326 Seconds

(without alignment)
2828.859 Million cell updates/sec

Title: US-09-970-076-8

Perfect score: 1728
Sequence: 1 MATERRALGIGFQWLSLST.....TTHCSLHKIASGPTTAACME 333

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1728	100.0	333	10	US-09-796-753-12
2	1728	100.0	333	14	US-10-038-307-2
3	1728	100.0	333	14	US-10-201-292-2
4	1728	100.0	564	14	US-10-038-307-20
5	1728	100.0	564	14	US-10-201-292-20
6	1728	99.4	564	14	US-10-038-307-24
7	1718	99.4	345	14	US-10-201-292-24
8	1713.5	99.2	342	14	US-10-038-307-22
9	1713.5	99.2	342	14	US-10-201-292-22
10	1650.5	95.5	551	14	US-10-038-307-18
11	1650.5	95.5	551	14	US-10-201-292-18
12	1649	95.4	564	11	US-09-833-245-621
13	1649	95.4	564	12	US-09-918-715-187
14	1649	95.4	564	12	US-09-918-715-232
15	1649	95.4	564	14	US-10-301-822-199

16	1649	95.4	564	16	US-10-408-765A-1823	Sequence 1823, App
17	1644	95.1	403	11	US-09-833-245-620	Sequence 620, App
18	1636	94.7	328	14	US-10-038-307-26	Sequence 26, App
19	1636	94.7	328	14	US-10-201-292-26	Sequence 26, App
20	1628	94.2	543	14	US-10-038-307-14	Sequence 14, App
21	1628	94.2	543	14	US-10-038-307-16	Sequence 16, App
22	1628	94.2	543	14	US-10-201-292-14	Sequence 14, App
23	1628	94.2	543	14	US-10-201-292-16	Sequence 16, App
24	1618	93.6	543	14	US-10-038-307-10	Sequence 10, App
25	1618	93.6	543	14	US-10-201-292-10	Sequence 10, App
26	1556	90.0	529	14	US-10-201-292-36	Sequence 36, App
27	1553	89.9	562	12	US-09-918-715-194	Sequence 194, App
28	1553	89.9	562	12	US-09-918-715-301	Sequence 301, App
29	1487	86.1	534	14	US-10-038-307-12	Sequence 12, App
30	1487	86.1	534	14	US-10-201-292-12	Sequence 12, App
31	1434.5	83.0	504	14	US-10-201-292-34	Sequence 34, App
32	1307	75.6	479	14	US-10-201-292-32	Sequence 32, App
33	1193	69.0	460	14	US-10-201-292-28	Sequence 28, App
34	1183	68.5	460	14	US-10-201-292-30	Sequence 30, App
35	903	52.3	538	13	US-10-047-542-99	Sequence 99, App
36	800.5	46.3	488	10	US-09-796-753-52	Sequence 52, App
37	800.5	46.3	488	14	US-10-038-307-6	Sequence 6, App
38	800.5	46.3	488	14	US-10-201-292-6	Sequence 6, App
39	800.5	46.3	488	14	US-10-368-087-16	Sequence 16, App
40	800.5	46.3	488	15	US-10-104-047-2639	Sequence 2639, App
41	785.5	45.5	587	9	US-09-764-870-312	Sequence 312, App
42	785.5	45.5	587	11	US-09-764-875-968	Sequence 968, App
43	785.5	45.5	587	14	US-10-125-540-312	Sequence 312, App
44	771	44.6	487	10	US-09-796-753-54	Sequence 54, App
45	771	44.6	487	14	US-10-038-307-8	Sequence 8, App

ALIGNMENTS

RESULT 1
US-09-796-753-12
Sequence 12, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USRS THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/365,164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/471,179
PRIOR FILING DATE: 1999-12-23

```

; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12

```

```

Query Match      100.0%; Score 1728; DB 10; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.3e-175;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPGACGPGDLYFLDKSGSVLHHMN 60
DB 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPGACGPGDLYFLDKSGSVLHHMN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRGLBELQKVLPGDPTM 120
DB 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRGLBELQKVLPGDPTM 120
QY 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
QY 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
QY 161 KDFNETQLARIADSKDHPVNDGFQALQGIHSHILKSCIEILAAEPSTICAGESFOVV 240
DB 161 KDFNETQLARIADSKDHPVNDGFQALQGIHSHILKSCIEILAAEPSTICAGESFOVV 240
QY 241 VRGNFPRHARNVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSMN 300
DB 241 VRGNFPRHARNVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSMN 300
QY 301 DGLSFISSSVITTTTHCSLHKIASGPTTAACME 333
DB 301 DGLSFISSSVITTTTHCSLHKIASGPTTAACME 333

```

```

RESULT 2
US-10-038-307-2
; Sequence 2, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038.307
; CURRENT FILING DATE: 2002-06-28

```

```

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-2

```

```

Query Match      100.0%; Score 1728; DB 14; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.3e-175;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPGACGPGDLYFLDKSGSVLHHMN 60
DB 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPGACGPGDLYFLDKSGSVLHHMN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRGLBELQKVLPGDPTM 120
DB 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRGLBELQKVLPGDPTM 120
QY 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
QY 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
QY 161 KDFNETQLARIADSKDHPVNDGFQALQGIHSHILKSCIEILAAEPSTICAGESFOVV 240
DB 161 KDFNETQLARIADSKDHPVNDGFQALQGIHSHILKSCIEILAAEPSTICAGESFOVV 240
QY 241 VRGNFPRHARNVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSMN 300
DB 241 VRGNFPRHARNVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSMN 300
QY 301 DGLSFISSSVITTTTHCSLHKIASGPTTAACME 333
DB 301 DGLSFISSSVITTTTHCSLHKIASGPTTAACME 333

```

```

RESULT 3
US-10-201-292-2
; Sequence 2, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201.292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-2

```

```

Query Match      100.0%; Score 1728; DB 14; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.3e-175;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPGACGPGDLYFLDKSGSVLHHMN 60
DB 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPGACGPGDLYFLDKSGSVLHHMN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRGLBELQKVLPGDPTM 120
DB 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRGLBELQKVLPGDPTM 120
QY 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
QY 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSDIGAIVYCVGV 180

```


QY 181 KDFNETOLARIADSKDHVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSPFOV 240
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/201,292
 ; CURRENT FILING DATE: 2003-02-14
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-201-292-20

Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSPFOV 240
 QY 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPEPSVEDTYLLCPAPILKEVGMKALQVSMN 300
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPEPSVEDTYLLCPAPILKEVGMKALQVSMN 300
 QY 301 DGLSFSSSVIITTHCSLHKIASGPTTAACME 333
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 301 DGLSFSSSVIITTHCSLHKIASGPTTAACME 333

RESULT 4
 ; Sequence 20, Application US/10038307
 ; Publication No. US20030134786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: James B. ROTTMAN
 ; APPLICANT: Theresa L. O'KEEFE
 ; APPLICANT: Engin OZKAYNAK
 ; APPLICANT: Judith J. HEALEY
 ; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Query Match 100.0%; Score 1728; DB 14; Length 564;
 Best Local Similarity 100.0%; Pred. No. 9.8e-175;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFQWLSLTLVLICAGGGRREDGPAICYGGFDLYFLIDSGSVLAHMN 60
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 1 MATERRALGIGFQWLSLTLVLICAGGGRREDGPAICYGGFDLYFLIDSGSVLAHMN 60
 QY 61 EIIYVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQIRQLEBELQKVLPGDPTM 120
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 61 EIIYVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQIRQLEBELQKVLPGDPTM 120
 QY 121 HEGFRASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYCYGV 180
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 121 HEGFRASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYCYGV 180
 QY 181 KDFNETOLARIADSKDHVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSPFOV 240
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSPFOV 240
 QY 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPEPSVEDTYLLCPAPILKEVGMKALQVSMN 300
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPEPSVEDTYLLCPAPILKEVGMKALQVSMN 300
 QY 301 DGLSFSSSVIITTHCSLHKIASGPTTAACME 333
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 301 DGLSFSSSVIITTHCSLHKIASGPTTAACME 333

RESULT 5
 ; Sequence 20, Application US/10201292
 ; Publication No. US2003014193A1
 ; GENERAL INFORMATION:
 ; APPLICANT: James B. ROTTMAN
 ; APPLICANT: Theresa L. O'KEEFE
 ; APPLICANT: Engin OZKAYNAK
 ; APPLICANT: Judith J. HEALEY

; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/201,292
 ; CURRENT FILING DATE: 2003-02-14
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-201-292-20

Query Match 100.0%; Score 1728; DB 14; Length 564;
 Best Local Similarity 100.0%; Pred. No. 9.8e-175;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFQWLSLTLVLICAGGGRREDGPAICYGGFDLYFLIDSGSVLAHMN 60
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 1 MATERRALGIGFQWLSLTLVLICAGGGRREDGPAICYGGFDLYFLIDSGSVLAHMN 60
 QY 61 EIIYVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQIRQLEBELQKVLPGDPTM 120
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 61 EIIYVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQIRQLEBELQKVLPGDPTM 120
 QY 121 HEGFRASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYCYGV 180
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 121 HEGFRASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYCYGV 180
 QY 181 KDFNETOLARIADSKDHVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSPFOV 240
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSPFOV 240
 QY 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPEPSVEDTYLLCPAPILKEVGMKALQVSMN 300
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPEPSVEDTYLLCPAPILKEVGMKALQVSMN 300
 QY 301 DGLSFSSSVIITTHCSLHKIASGPTTAACME 333
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-20

Db 301 DGLSFSSSVIITTHCSLHKIASGPTTAACME 333

RESULT 6
 ; Sequence 24, Application US/10038307
 ; Publication No. US20030134786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: James B. ROTTMAN
 ; APPLICANT: Theresa L. O'KEEFE
 ; APPLICANT: Engin OZKAYNAK
 ; APPLICANT: Judith J. HEALEY
 ; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-24

Query Match 99.4%; Score 1718; DB 14; Length 345;
 Best Local Similarity 99.7%; Pred. No. 5.3e-174;
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATERRALGIGFQWLSLTLVLICAGGGRREDGPAICYGGFDLYFLIDSGSVLAHMN 60
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-24

Db 1 MATERRALGIGFQWLSLTLVLICAGGGRREDGPAICYGGFDLYFLIDSGSVLAHMN 60
 QY 61 EIIYVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQIRQLEBELQKVLPGDPTM 120
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/038,307
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-038-307-24

Db 61 EIIYVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTEDREQIRQLEBELQKVLPGDPTM 120

QY 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSEERANRSDIGAIYVCV 180
| | | | |
Db 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSEERANRSDIGAIYVCV 180
QY 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEILAAEPSTICAGESFOV 240
| | | | |
Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEILAAEPSTICAGESFOV 240
QY 241 VRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
| | | | |
Db 241 VRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
QY 301 DGLSFSSSVIITTHCSLHKIASGPTTAACME 333
| | | | |
Db 301 DGLSFSSSVIITTHCSLHKIASGPTTAACME 333

RESULT 7

US-10-201-292-24
; Sequence 24, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201.292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-24

Query Match 99.4%; Score 1718; DB 14; Length 345;
Best Local Similarity 99.7%; Pred. No. 5.3e-174;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHNMN 60
| | | | |
Db 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHNMN 60
QY 61 EIIYFVEQLAHKFISSPOLRMSFIVFSTRGTTLMKLTEDREQIROGLEELQVLPFGDTYM 120
| | | | |
Db 61 EIIYFVEQLAHKFISSPOLRMSFIVFSTRGTTLMKLTEDREQIROGLEELQVLPFGDTYM 120
QY 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSEERANRSDIGAIYVCV 180
| | | | |
Db 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSEERANRSDIGAIYVCV 180
QY 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEILAAEPSTICAGESFOV 240
| | | | |
Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEILAAEPSTICAGESFOV 240
QY 241 VRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
| | | | |
Db 241 VRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
QY 301 DGLSFSSSVIITTHCSLHKIASGPTTAACME 333
| | | | |
Db 301 DGLSFSSSVIITTHCSLHKIASGPTTAACME 333

RESULT 8
US-10-038-307-22
; Sequence 22, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:

; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038.307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-22

Query Match 99.2%; Score 1713.5; DB 14; Length 342;
Best Local Similarity 97.4%; Pred. No. 1.6e-173;
Matches 333; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGACGFDLYFILDK 51
| | | | |
Db 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGMDYKDDDKACYGFDLYFILDK 60
QY 52 SGSVLHNMNIYFVEQLAHKFISSPOLRMSFIVFSTRGTTLMKLTEDREQIROGLEELQ 111
| | | | |
Db 61 SGSVLHNMNIYFVEQLAHKFISSPOLRMSFIVFSTRGTTLMKLTEDREQIROGLEELQ 120
QY 112 VLPFGDTYMHEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSEERANRSD 171
| | | | |
Db 121 VLPFGDTYMHEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSEERANRSD 180
QY 172 GAIYVCVNDPNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEILAAEPSTI 231
| | | | |
Db 181 GAIYVCVNDPNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEILAAEPSTI 240
QY 232 CAGESFOVVRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVG 291
| | | | |
Db 241 CAGESFOVVRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVG 300
QY 292 KAALQVSMNDGLSFSSSVIITTHCSLHKIASGPTTAACME 333
| | | | |
Db 301 KAALQVSMNDGLSFSSSVIITTHCSLHKIASGPTTAACME 342

RESULT 9

US-10-201-292-22
; Sequence 22, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201.292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-22

Query Match 99.2%; Score 1713.5; DB 14; Length 342;
Best Local Similarity 97.4%; Pred. No. 1.6e-173;
Matches 333; Conservative 0; Mismatches 0; Indels 9; Gaps 1;
QY 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGACGFDLYFILDK 51
| | | | |
Db 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGMDYKDDDKACYGFDLYFILDK 60

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QY 52 SSVLHNNHNIYFVEQLAHKFIISPOLRMSPIVSTRGTTLMKLTEDREQIROLGEBLQK 111
DB 61 SSVLHNNHNIYFVEQLAHKFIISPOLRMSPIVSTRGTTLMKLTEDREQIROLGEBLQK 120
QY 112 VLPGGDTYMHGGERASQIYYENRGYRTASVIALTDGELHEDLPFYSERENRSD 171
DB 121 VLPGGDTYMHGGERASQIYYENRGYRTASVIALTDGELHEDLPFYSERENRSD 180
QY 172 GAIYVCVGVKDFNETOLARIADSKDHPVNDGFOALOGIHSILKSCIEIIAEPSTI 231
DB 181 GAIYVCVGVKDFNETOLARIADSKDHPVNDGFOALOGIHSILKSCIEIIAEPSTI 240
QY 232 CAGESFOVYVVRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGM 291
DB 241 CAGESFOVYVVRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGM 300
QY 292 KALQVSNMDGLSPFISSSVIITTHCSLHKIASGPTTAA 333
DB 301 KALQVSNMDGLSPFISSSVIITTHCSLHKIASGPTTAA 342

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RESULT 10

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US-10-038-307-18
; Sequence 18, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-18

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Query Match 95.5%; Score 1650.5; DB 14; Length 551;
Best Local Similarity 97.3%; Pred. No. 1.7e-166;
Matches 320; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

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QY 1 MATARRALGIGFOWLSLTLVILICAGGGRREDGPAFCYGGFDLYFIIDKSGSVLHNN 60
DB 1 MATARRALGIGFOWLSLTLVILICAGGGRREDGPAFCYGGFDLYFIIDKSGSVLHNN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSPIVSTRGTTLMKLTEDREQIROLGEBLQK 120
DB 61 EIIYFVEQLAHKFIISPOLRMSPIVSTRGTTLMKLTEDREQIROLGEBLQK 120
QY 121 HEGFERASQIYYENRGYRTASVIALTDGELHEDLPFYSERENRSD 180
DB 121 HEGFERASQIYYENRGYRTASVIALTDGELHEDLPFYSERENRSD 180
QY 181 KOFNETOLARIADSKDHPVNDGFOALOGIHSILKSCIEIIAEPSTI 240
DB 181 KOFNETOLARIADSKDHPVNDGFOALOGIHSILKSCIEIIAEPSTI 240
QY 241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGM 300
DB 241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGM 300
QY 301 DGLSFISSSVIITTHCSLHKIASGPTTAA 329
DB 301 DGLSFISSSVIITTHCSLHKIASGPTTAA 324

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RESULT 11

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US-10-201-292-18
; Sequence 18, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-18

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Query Match 95.5%; Score 1650.5; DB 14; Length 551;
Best Local Similarity 97.3%; Pred. No. 1.7e-166;
Matches 320; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

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QY 1 MATARRALGIGFOWLSLTLVILICAGGGRREDGPAFCYGGFDLYFIIDKSGSVLHNN 60
DB 1 MATARRALGIGFOWLSLTLVILICAGGGRREDGPAFCYGGFDLYFIIDKSGSVLHNN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSPIVSTRGTTLMKLTEDREQIROLGEBLQK 120
DB 61 EIIYFVEQLAHKFIISPOLRMSPIVSTRGTTLMKLTEDREQIROLGEBLQK 120
QY 121 HEGFERASQIYYENRGYRTASVIALTDGELHEDLPFYSERENRSD 180
DB 121 HEGFERASQIYYENRGYRTASVIALTDGELHEDLPFYSERENRSD 180
QY 181 KOFNETOLARIADSKDHPVNDGFOALOGIHSILKSCIEIIAEPSTI 240
DB 181 KOFNETOLARIADSKDHPVNDGFOALOGIHSILKSCIEIIAEPSTI 240
QY 241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGM 300
DB 241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGM 300
QY 301 DGLSFISSSVIITTHCSLHKIASGPTTAA 329
DB 301 DGLSFISSSVIITTHCSLHKIASGPTTAA 324

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RESULT 12
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621

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Query Match 95.4%; Score 1649; DB 11; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.5e-166;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPAICYGFPDLYFLIDKSGSVLHHMN 60
DB 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPAICYGFPDLYFLIDKSGSVLHHMN 60
QY 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120
DB 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120
QY 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIVYCVGV 180
DB 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIVYCVGV 180
QY 181 KDFNETOLARIADSKDHVPVNDGFQALOGIIHSILKSCIEIIAEPSTTCAGESFQV 240
DB 181 KDFNETOLARIADSKDHVPVNDGFQALOGIIHSILKSCIEIIAEPSTTCAGESFQV 240
QY 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSDTYLLCPAPILKEVGKALQVSMN 300
DB 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSDTYLLCPAPILKEVGKALQVSMN 300
QY 301 DGLSFSSSVIITTTTHCS 318
DB 301 DGLSFSSSVIITTTTHCS 318

RESULT 13
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-187

Query Match 95.4%; Score 1649; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 2.6e-166;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPAICYGFPDLYFLIDKSGSVLHHMN 60
DB 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPAICYGFPDLYFLIDKSGSVLHHMN 60
QY 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120
DB 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120
QY 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIVYCVGV 180
DB 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIVYCVGV 180
QY 181 KDFNETOLARIADSKDHVPVNDGFQALOGIIHSILKSCIEIIAEPSTTCAGESFQV 240
DB 181 KDFNETOLARIADSKDHVPVNDGFQALOGIIHSILKSCIEIIAEPSTTCAGESFQV 240

DB 181 KDFNETOLARIADSKDHVPVNDGFQALOGIIHSILKSCIEIIAEPSTTCAGESFQV 240
QY 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSDTYLLCPAPILKEVGKALQVSMN 300
DB 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSDTYLLCPAPILKEVGKALQVSMN 300
QY 301 DGLSFSSSVIITTTTHCS 318
DB 301 DGLSFSSSVIITTTTHCS 318

RESULT 14
US-09-918-715-232
; Sequence 232, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-232

Query Match 95.4%; Score 1649; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 2.6e-166;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPAICYGFPDLYFLIDKSGSVLHHMN 60
DB 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPAICYGFPDLYFLIDKSGSVLHHMN 60
QY 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120
DB 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120
QY 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIVYCVGV 180
DB 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIVYCVGV 180
QY 181 KDFNETOLARIADSKDHVPVNDGFQALOGIIHSILKSCIEIIAEPSTTCAGESFQV 240
DB 181 KDFNETOLARIADSKDHVPVNDGFQALOGIIHSILKSCIEIIAEPSTTCAGESFQV 240
QY 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSDTYLLCPAPILKEVGKALQVSMN 300
DB 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSDTYLLCPAPILKEVGKALQVSMN 300
QY 301 DGLSFSSSVIITTTTHCS 318
DB 301 DGLSFSSSVIITTTTHCS 318

RESULT 15
US-10-301-822-199
; Sequence 199, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berge, Allison

APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-0292RNM
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 199
LENGTH: 564
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-301-822-199

Query Match 95.4%; Score 1649; DB 14; Length 564;
Best Local Similarity 100.0%; Pred. No. 2.6e-166;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATARRALGIGFOMLSLATLVLCAGCGGRRDGGPACYGFPDLYFILDKSGSVLHHMN 60
DB 1 MATARRALGIGFOMLSLATLVLCAGCGGRRDGGPACYGFPDLYFILDKSGSVLHHMN 60
QY 61 EIYFVEQLAHKFIISPOLMSFIVSTRGTTLMKLTEDREQIRQGLBELQKVLPGSDTYM 120
DB 61 EIYFVEQLAHKFIISPOLMSFIVSTRGTTLMKLTEDREQIRQGLBELQKVLPGSDTYM 120
QY 121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLPFYSEREANRSRDLCATYCVGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLPFYSEREANRSRDLCATYCVGV 180
QY 181 KOFNETQLARINDSKDHVPVNDGFOALQGIHSHILKKSCEIILAEPESTICAGESFOVY 240
DB 181 KOFNETQLARINDSKDHVPVNDGFOALQGIHSHILKKSCEIILAEPESTICAGESFOVY 240
QY 241 VRGNFRRHARNVDRVLCSEFKINDSVTLNEKPPSVEEDTYLLCPAPILKEVGMKALQVSMN 300
DB 241 VRGNFRRHARNVDRVLCSEFKINDSVTLNEKPPSVEEDTYLLCPAPILKEVGMKALQVSMN 300
QY 301 DGLSFISSSVITTTTHCS 318
DB 301 DGLSFISSSVITTTTHCS 318

Search completed: June 21, 2004, 14:02:14
Job time : 34.2326 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 13:44:26 ; Search time 56.2859 Seconds

(without alignments)
2828.859 Million cell updates/sec

Title: US-09-970-076-6

Perfect score: 3025
Sequence: 1 MATERRRLGIGFQWLSLAT.....QAPPNPAPPPSPPPSPV 564

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3025	100.0	564	12	US-09-918-715-187
2	3025	100.0	564	12	US-09-918-715-232
3	3025	100.0	564	14	US-10-301-832-199
4	3025	100.0	564	16	US-10-408-765A-1823
5	2901	95.9	562	12	US-09-918-715-194
6	2901	95.9	562	12	US-09-918-715-301
7	2017	66.7	381	10	US-09-796-753-24
8	2017	66.7	381	14	US-10-038-307-4
9	2017	66.7	381	14	US-10-201-292-4
10	1893.5	62.6	403	11	US-09-833-245-621
11	1874	62.0	403	11	US-09-833-245-620
12	1661	54.9	551	14	US-10-038-307-18
13	1661	54.9	551	14	US-10-201-292-18
14	1649	54.5	333	10	US-09-796-753-12
15	1649	54.5	333	14	US-10-038-307-2

16	1649	54.5	333	14	US-10-201-292-2	Sequence 2, Appli
17	1649	54.5	345	14	US-10-038-307-24	Sequence 24, Appl
18	1649	54.5	345	14	US-10-201-292-24	Sequence 24, Appl
19	1649	54.5	564	14	US-10-038-307-20	Sequence 20, Appl
20	1649	54.5	564	14	US-10-038-307-20	Sequence 20, Appl
21	1636	54.1	328	14	US-10-038-307-26	Sequence 26, Appl
22	1636	54.1	328	14	US-10-038-307-26	Sequence 26, Appl
23	1634.5	54.0	342	14	US-10-038-307-22	Sequence 22, Appl
24	1634.5	54.0	342	14	US-10-201-292-22	Sequence 22, Appl
25	1629	53.9	543	14	US-10-038-307-14	Sequence 14, Appl
26	1629	53.9	543	14	US-10-038-307-16	Sequence 16, Appl
27	1629	53.9	543	14	US-10-201-292-14	Sequence 14, Appl
28	1629	53.9	543	14	US-10-201-292-16	Sequence 16, Appl
29	1619	53.5	543	14	US-10-038-307-10	Sequence 10, Appl
30	1619	53.5	543	14	US-10-201-292-10	Sequence 10, Appl
31	1552.5	51.3	529	14	US-10-201-292-36	Sequence 36, Appl
32	1488	49.2	534	14	US-10-038-307-12	Sequence 12, Appl
33	1488	49.2	534	14	US-10-201-292-12	Sequence 12, Appl
34	1434.5	47.4	504	14	US-10-201-292-34	Sequence 34, Appl
35	1416.5	46.8	488	14	US-10-368-087-16	Sequence 16, Appl
36	1416.5	46.8	488	15	US-10-104-047-2639	Sequence 2639, Ap
37	1411.5	46.7	488	10	US-09-796-753-52	Sequence 52, Appl
38	1411.5	46.7	488	14	US-10-038-307-6	Sequence 6, Appl
39	1411.5	46.7	488	14	US-10-201-292-6	Sequence 6, Appl
40	1396.5	46.2	487	10	US-09-796-753-54	Sequence 54, Appl
41	1396.5	46.2	487	14	US-10-038-307-8	Sequence 8, Appl
42	1396.5	46.2	487	14	US-10-201-292-8	Sequence 8, Appl
43	1396.5	46.2	487	14	US-10-368-087-15	Sequence 15, Appl
44	1307	43.2	479	14	US-10-201-292-32	Sequence 32, Appl
45	1206.5	39.9	587	9	US-09-764-870-312	Sequence 312, Appl

ALIGNMENTS

RESULT 1
US-09-918-715-187
Sequence 187, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT FILING DATE: US/09/918, 715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 187
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
US-09-918-715-187

Query Match 100.0%; Score 3025; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 3.7e-225; Indels 0; Gaps 0;
Matches 564; Conservative 0;

QY 1 MATERRRLGIGFQWLSLATVILICAGGGRREDGPAFCYGFPLYFLIDKSGSVLHNM 60
DB 1 MATERRRLGIGFQWLSLATVILICAGGGRREDGPAFCYGFPLYFLIDKSGSVLHNM 60
QY 61 EIVYVEQLAHKFISPOLRMSFIYFSTRTTLMKLTEDREOIRQCLBELQKVLPGSDTYM 120
DB 61 EIVYVEQLAHKFISPOLRMSFIYFSTRTTLMKLTEDREOIRQCLBELQKVLPGSDTYM 120

Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFPYSEBRANRSDGAIIVYCVG 180
Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFPYSEBRANRSDGAIIVYCVG 180
Qy 181 KDFNETOLARIADSKDHFVFNVDGFOALOGIIHSLTKKSCIEILAAEPSTICAGESFOV 240
Db 181 KDFNETOLARIADSKDHFVFNVDGFOALOGIIHSLTKKSCIEILAAEPSTICAGESFOV 240
Qy 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSVDYLLCPAPILKEVGKALQVSMN 300
Db 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSVDYLLCPAPILKEVGKALQVSMN 300
Qy 301 DGLSFSSSVIITTHCSDSIIAIALIIFLLAIALLMFWPLCCTVIIKEVPPPAE 360
Db 301 DGLSFSSSVIITTHCSDSIIAIALIIFLLAIALLMFWPLCCTVIIKEVPPPAE 360
Qy 361 ESEBEDDGLPKKMPVTDASYGGRGVGIIKMEVWGEKSTEBGAKLEKANAAYKM 420
Db 361 ESEBEDDGLPKKMPVTDASYGGRGVGIIKMEVWGEKSTEBGAKLEKANAAYKM 420
Qy 421 PEOEYEPPEPRNLNNMRSPSPRKWSPYIKGLDALMVLARKGYDRSVMRPOGDTGR 480
Db 421 PEOEYEPPEPRNLNNMRSPSPRKWSPYIKGLDALMVLARKGYDRSVMRPOGDTGR 480
Qy 481 CINFRVKNQOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPSTL 540
Db 481 CINFRVKNQOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPSTL 540
Qy 541 PPPQAPPNNRAPPSPRPPPSV 564
Db 541 PPPQAPPNNRAPPSPRPPPSV 564

RESULT 2

US-09-918-715-232
; Sequence 232, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT FILING DATE: 2001-08-01
; PRIOR FILING DATE: 2000-06-02
; PRIOR FILING DATE: 2000-06-02
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-232

Query Match 100.0%; Score 3025; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 3,7e-225;
Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATARRALGIGFQWLSLATVLIICAGGGRREDGPGACGGFDLYFTLDKSGSVLHHMN 60
Db 1 MATARRALGIGFQWLSLATVLIICAGGGRREDGPGACGGFDLYFTLDKSGSVLHHMN 60
Qy 61 EIIYFVEQLAHKFISPOLRMSFIVFSTRTTLMKLTEDREQIRQGLELOKVLPGDPTYM 120
Db 61 EIIYFVEQLAHKFISPOLRMSFIVFSTRTTLMKLTEDREQIRQGLELOKVLPGDPTYM 120
Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFPYSEBRANRSDGAIIVYCVG 180
Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFPYSEBRANRSDGAIIVYCVG 180

Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFPYSEBRANRSDGAIIVYCVG 180
Qy 181 KDFNETOLARIADSKDHFVFNVDGFOALOGIIHSLTKKSCIEILAAEPSTICAGESFOV 240
Db 181 KDFNETOLARIADSKDHFVFNVDGFOALOGIIHSLTKKSCIEILAAEPSTICAGESFOV 240
Qy 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSVDYLLCPAPILKEVGKALQVSMN 300
Db 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSVDYLLCPAPILKEVGKALQVSMN 300
Qy 301 DGLSFSSSVIITTHCSDSIIAIALIIFLLAIALLMFWPLCCTVIIKEVPPPAE 360
Db 301 DGLSFSSSVIITTHCSDSIIAIALIIFLLAIALLMFWPLCCTVIIKEVPPPAE 360
Qy 361 ESEBEDDGLPKKMPVTDASYGGRGVGIIKMEVWGEKSTEBGAKLEKANAAYKM 420
Db 361 ESEBEDDGLPKKMPVTDASYGGRGVGIIKMEVWGEKSTEBGAKLEKANAAYKM 420
Qy 421 PEOEYEPPEPRNLNNMRSPSPRKWSPYIKGLDALMVLARKGYDRSVMRPOGDTGR 480
Db 421 PEOEYEPPEPRNLNNMRSPSPRKWSPYIKGLDALMVLARKGYDRSVMRPOGDTGR 480
Qy 481 CINFRVKNQOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPSTL 540
Db 481 CINFRVKNQOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPSTL 540
Qy 541 PPPQAPPNNRAPPSPRPPPSV 564
Db 541 PPPQAPPNNRAPPSPRPPPSV 564

RESULT 3

US-10-301-822-199
; Sequence 199, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT FILING DATE: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-199

Query Match 100.0%; Score 3025; DB 14; Length 564;
Best Local Similarity 100.0%; Pred. No. 3,7e-225;
Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATARRALGIGFQWLSLATVLIICAGGGRREDGPGACGGFDLYFTLDKSGSVLHHMN 60
Db 1 MATARRALGIGFQWLSLATVLIICAGGGRREDGPGACGGFDLYFTLDKSGSVLHHMN 60
Qy 61 EIIYFVEQLAHKFISPOLRMSFIVFSTRTTLMKLTEDREQIRQGLELOKVLPGDPTYM 120
Db 61 EIIYFVEQLAHKFISPOLRMSFIVFSTRTTLMKLTEDREQIRQGLELOKVLPGDPTYM 120


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Db      ||| 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCV 180
Qy      ||| 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCV 180
Db      ||| 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCV 180
Qy      ||| 181 KDFNETOLARIADSKDHFVPNDGFQALOGIIHSLKKSCEIILAEBSSTICAGESFOV 240
Db      ||| 181 KDFNETOLARIADSKDHFVPNDGFQALOGIIHSLKKSCEIILAEBSSTICAGESFOV 240
Qy      ||| 241 VRNGFRRARNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPLKEVGKALQVSMN 300
Db      ||| 241 VRNGFRRARNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPLKEVGKALQVSMN 300
Qy      ||| 301 DGLSFISSSVITTTTHCSGDSIIALAILFLALALMMFWPLCTCVIIKEVPPPAE 360
Db      ||| 301 DGLSFISSSVITTTTHCSGDSIIALAILFLALALMMFWPLCTCVIIKEVPPPAE 360
Qy      ||| 361 ESEEDDDGLPKKKMPTVDASYGGRGVGIGKMEVWGEKSTEGAKLEKAKARVYM 420
Db      ||| 361 ESEEDDDGLPKKKMPTVDASYGGRGVGIGKMEVWGEKSTEGAKLEKAKARVYM 420
Qy      ||| 421 PEOEYEPERPNLNNMRPSSPRKWSPIKGLDALWVLKGYDRSVNRPQGDIGR 480
Db      ||| 421 PEOEYEPERPNLNNMRPSSPRKWSPIKGLDALWVLKGYDRSVNRPQGDIGR 480
Qy      ||| 481 CINFTRVKNQPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSBSTL 540
Db      ||| 481 CINFTRVKNQPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSBSTL 540
Qy      ||| 541 PPPQAPPNRAPPSRPPPSV 564
Db      ||| 541 PPPQAPPNRAPPSRPPPSV 564

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RESULT 4

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US-10-408-765A-1823
; Sequence 1823, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408.765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1823
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1823

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Query Match      100.0%; Score 3025; DB 16; Length 564;
Best Local Similarity 100.0%; Pred. No. 3.7e-225;
Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 NATAERRALGIGFOWLSLTLVLICAGCGRRDGGPACGFDLYFIIDKSGSVLHNN 60
Db      1 NATAERRALGIGFOWLSLTLVLICAGCGRRDGGPACGFDLYFIIDKSGSVLHNN 60
Qy      61 EIIYVEQALAHKFISPOLMSFIVSTRGTTLMKLTEDREQIRQGLELOKVLPGDITVM 120
Db      61 EIIYVEQALAHKFISPOLMSFIVSTRGTTLMKLTEDREQIRQGLELOKVLPGDITVM 120

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Qy      ||| 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCV 180
Db      ||| 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCV 180
Qy      ||| 181 KDFNETOLARIADSKDHFVPNDGFQALOGIIHSLKKSCEIILAEBSSTICAGESFOV 240
Db      ||| 181 KDFNETOLARIADSKDHFVPNDGFQALOGIIHSLKKSCEIILAEBSSTICAGESFOV 240
Qy      ||| 241 VRNGFRRARNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPLKEVGKALQVSMN 300
Db      ||| 241 VRNGFRRARNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPLKEVGKALQVSMN 300
Qy      ||| 301 DGLSFISSSVITTTTHCSGDSIIALAILFLALALMMFWPLCTCVIIKEVPPPAE 360
Db      ||| 301 DGLSFISSSVITTTTHCSGDSIIALAILFLALALMMFWPLCTCVIIKEVPPPAE 360
Qy      ||| 361 ESEEDDDGLPKKKMPTVDASYGGRGVGIGKMEVWGEKSTEGAKLEKAKARVYM 420
Db      ||| 361 ESEEDDDGLPKKKMPTVDASYGGRGVGIGKMEVWGEKSTEGAKLEKAKARVYM 420
Qy      ||| 421 PEOEYEPERPNLNNMRPSSPRKWSPIKGLDALWVLKGYDRSVNRPQGDIGR 480
Db      ||| 421 PEOEYEPERPNLNNMRPSSPRKWSPIKGLDALWVLKGYDRSVNRPQGDIGR 480
Qy      ||| 481 CINFTRVKNQPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSBSTL 540
Db      ||| 481 CINFTRVKNQPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSBSTL 540
Qy      ||| 541 PPPQAPPNRAPPSRPPPSV 564
Db      ||| 541 PPPQAPPNRAPPSRPPPSV 564

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RESULT 5

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US-09-918-715-194
; Sequence 194, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918.715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 194
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-194

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Query Match      95.9%; Score 2901; DB 12; Length 562;
Best Local Similarity 96.8%; Pred. No. 1.4e-215;
Matches 538; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
Qy      9 LGIGFOWLSLTLVLICAGCGRRDGGPACGFDLYFIIDKSGSVLHNNIYFVEQ 68
Db      7 LGAGRGICVALALVLCAGHGRREDGGPACGFDLYFIIDKSGSVLHNNIYFVEQ 66
Qy      69 LAHRTISPOLMSFIVSTRGTTLMKLTEDREQIRQGLELOKVLPGDITVMHSEFERAS 128
Db      67 LAHRTISPOLMSFIVSTRGTTLMKLTEDREQIRQGLELOKVLPGDITVMHSEFERAS 126
Qy      129 EOIYVENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVQDFNETOL 188
Db      129 EOIYVENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVQDFNETOL 188

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Db 127 EQIYVENSQGYRTASVITLALTDGELHEDLFFYSEREANRSDLGAIVYCVGKDFNETOL 186
Qy 189 ARIADSKDHVPFVNDGFQALOGIHSILKSCIEIIIAEPSTICAGESFOVVVWNGNGFRH 248
Db 187 ARIADSKDHVPFVNDGFQALOGIHSILKSCIEIIIAEPSTICAGESFOVVVWNGNGFRH 246
Qy 249 ARNDRVLCSPKINDSVTLNEKPEFVADTYLLCPAPILKEVGMKAAQVSNNDGLSFTSS 308
Db 247 ARNDRVLCSPKINDSVTLNEKPEFVADTYLLCPAPILKEVGMKAAQVSNNDGLSFTSS 306
Qy 309 SVITTTTCSDGSIATLALILFLLLALALLMMFWPLCTCTVIIEVPPPAEESSEEDDD 368
Db 307 SVITTTTCSDGSIATLALILFLLLALALLMMFWPLCTCTVIIEVPPPAEESSEEDDD 366
Qy 369 GLPKKKMPTVDASYGGRGVGGIKRMEVRWGEKSTEGALKLEKAKARVAMPQOEYFEP 428
Db 367 GLPKKKMPTVDASYGGRGVGGIKRMEVRWGEKSTEGALKLEKAKARVAMPQOEYFEP 426
Qy 429 EPRNLNNMRRPSSPRKMYSPIKGKLDALWVLLRKGYDRVSVMRPOGDTGRCINFTRVK 488
Db 427 EPRNLNNMRRPSSPRKMYSPIKGKLDALWVLLRKGYDRVSVMRPOGDTGRCINFTRVK 486
Qy 489 NNOPAKYPLNNAHYTSSPPAPITYTPPPAPHCPPPPSAPTPPIPSBSTLPPPPQAPP 548
Db 487 NSQPAKYPLNNTYHSSPPAPITYTPPPAPHCPPPPSAPTPPIPSBSTLPPPPQAPP 546
Qy 549 PNRAAPPSPRPPPSV 564
Db 547 PNRAAPPSPRPPPSV 562

RESULT 6
US-09-918-715-301
; Sequence 301, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mouse
US-09-918-715-301

Query Match 95.9%; Score 2901; DB 12; Length 562;
Best Local Similarity 96.8%; Pred. No. 1.4e-215;
Matches 538; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 9 LGIGFQWMLATLVLIICAGCGRRREDGGPACYGFDLYFLIDKSGSVLHNNNEIYYVEQ 68
Db 7 LGAGRGCAVALVLCAGHGRRREDGGPACYGFDLYFLIDKSGSVLHNNNEIYYVEQ 66
Qy 69 LAHKISQOLMSFVSTRTGTTLMKLTEDRBOIRQGLEBIQKVLPGSDTYMHGFERAS 128
Db 67 LAHRISQOLMSFVSTRTGTTLMKLTEDRBOIRQGLEBIQKVLPGSDTYMHGFERAS 126
Qy 129 EQIYVENSQGYRTASVITLALTDGELHEDLFFYSEREANRSDLGAIVYCVGKDFNETOL 188
Db 127 EQIYVENSQGYRTASVITLALTDGELHEDLFFYSEREANRSDLGAIVYCVGKDFNETOL 186

Qy 189 ARIADSKDHVPFVNDGFQALOGIHSILKSCIEIIIAEPSTICAGESFOVVVWNGNGFRH 248
Db 187 ARIADSKDHVPFVNDGFQALOGIHSILKSCIEIIIAEPSTICAGESFOVVVWNGNGFRH 246
Qy 249 ARNDRVLCSPKINDSVTLNEKPEFVADTYLLCPAPILKEVGMKAAQVSNNDGLSFTSS 308
Db 247 ARNDRVLCSPKINDSVTLNEKPEFVADTYLLCPAPILKEVGMKAAQVSNNDGLSFTSS 306
Qy 309 SVITTTTCSDGSIATLALILFLLLALALLMMFWPLCTCTVIIEVPPPAEESSEEDDD 368
Db 307 SVITTTTCSDGSIATLALILFLLLALALLMMFWPLCTCTVIIEVPPPAEESSEEDDD 366
Qy 369 GLPKKKMPTVDASYGGRGVGGIKRMEVRWGEKSTEGALKLEKAKARVAMPQOEYFEP 428
Db 367 GLPKKKMPTVDASYGGRGVGGIKRMEVRWGEKSTEGALKLEKAKARVAMPQOEYFEP 426
Qy 429 EPRNLNNMRRPSSPRKMYSPIKGKLDALWVLLRKGYDRVSVMRPOGDTGRCINFTRVK 488
Db 427 EPRNLNNMRRPSSPRKMYSPIKGKLDALWVLLRKGYDRVSVMRPOGDTGRCINFTRVK 486
Qy 489 NNOPAKYPLNNAHYTSSPPAPITYTPPPAPHCPPPPSAPTPPIPSBSTLPPPPQAPP 548
Db 487 NSQPAKYPLNNTYHSSPPAPITYTPPPAPHCPPPPSAPTPPIPSBSTLPPPPQAPP 546
Qy 549 PNRAAPPSPRPPPSV 564
Db 547 PNRAAPPSPRPPPSV 562

RESULT 7
US-09-796-753-24
; Sequence 24, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25

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; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 24
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Mouse
US-09-796-753-24

```

Query Match 66.7%; Score 2017; DB 10; Length 381;

Best Local Similarity 98.1%; Pred. No. 1.9e-147; Indels 0; Gaps 0;

Matches 371; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 187 QIARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFQVVRGNGF 246
DB 4 QIARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFQVVRGNGF 63
QY 247 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 306
DB 64 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 123
QY 307 SSSVITTTTHCSDSIIAIIALLIFLLALALLMFWPFLCCTVIIKEVPPPAEESBED 366
DB 124 SSSVITTTTHCSDSIIAIIALLIFLLALALLMFWPFLCCTVIIKEVPPPAEESBED 183
QY 367 DDGLPKKKMPTVDASYGGRGVGIGKMEVWGEKSTEBGAKLEKANNARVKMPEOYE 426
DB 184 DDGLPKKKMPTVDASYGGRGVGIGKMEVWGEKSTEBGAKLEKANNARVKMPEOYE 243
QY 427 FPEPNLNMMNRSPSPKMWSPKIGKLDALMWLRLKGYDRVSVMRPOGDTGRCINFTR 486
DB 244 FPEPNLNMMNRSPSPKMWSPKIGKLDALMWLRLKGYDRVSVMRPOGDTGRCINFTR 303
QY 487 VKNQOPAKYPLNNAYHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPTLPPPOA 546
DB 304 VKNQOPAKYPLNNAYHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPTLPPPOA 363
QY 547 PPNRAPPSPRPPPSV 564
DB 364 PPNRAPPSPRPPPSV 381

```

```

RESULT 8
US-10-038-307-4
; Sequence 4, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 4
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Murine
US-10-038-307-4

```

Query Match 66.7%; Score 2017; DB 14; Length 381;

Best Local Similarity 98.1%; Pred. No. 1.9e-147; Indels 0; Gaps 0;

Matches 371; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 187 QIARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFQVVRGNGF 246
DB 4 QIARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFQVVRGNGF 63
QY 247 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 306
DB 64 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 123
QY 307 SSSVITTTTHCSDSIIAIIALLIFLLALALLMFWPFLCCTVIIKEVPPPAEESBED 366
DB 124 SSSVITTTTHCSDSIIAIIALLIFLLALALLMFWPFLCCTVIIKEVPPPAEESBED 183
QY 367 DDGLPKKKMPTVDASYGGRGVGIGKMEVWGEKSTEBGAKLEKANNARVKMPEOYE 426
DB 184 DDGLPKKKMPTVDASYGGRGVGIGKMEVWGEKSTEBGAKLEKANNARVKMPEOYE 243
QY 427 FPEPNLNMMNRSPSPKMWSPKIGKLDALMWLRLKGYDRVSVMRPOGDTGRCINFTR 486
DB 244 FPEPNLNMMNRSPSPKMWSPKIGKLDALMWLRLKGYDRVSVMRPOGDTGRCINFTR 303
QY 487 VKNQOPAKYPLNNAYHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPTLPPPOA 546
DB 304 VKNQOPAKYPLNNAYHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPTLPPPOA 363
QY 547 PPNRAPPSPRPPPSV 564
DB 364 PPNRAPPSPRPPPSV 381

```

```

RESULT 9
US-10-201-292-4
; Sequence 4, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Murine
US-10-201-292-4

```

Query Match 66.7%; Score 2017; DB 14; Length 381;

Best Local Similarity 98.1%; Pred. No. 1.9e-147; Indels 0; Gaps 0;

Matches 371; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 187 QIARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFQVVRGNGF 246
DB 4 QIARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFQVVRGNGF 63
QY 247 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 306
DB 64 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 123
QY 307 SSSVITTTTHCSDSIIAIIALLIFLLALALLMFWPFLCCTVIIKEVPPPAEESBED 366

```

Db	124	SSSVIITTHCSGSGSLTALTLVLFLTLTALLMMFWPLCCVITIKVPPPPVSESEED	183
Qy	367	DDGLPKKKMTVYASTYGGRGVGIGIKRMVRNGEKGSTBEQAKLFKANNAVKNPBE0YE	426
Db	184	DDGLPKKKMTVYASTYGGRGVGIGIKRMVRNGEKGSTBEQAKLEKANNAVKNPBE0YE	243
Qy	427	FPFERNLNNMRRPSSSPRKWYSPBIIKKGLDALVLLRKGYDRVSVVRPQPGDTGRCINFTR	466
Db	244	FPFERNLNNMRRPSSSPRKWYSPBIIKKGLDALVLLRKGYDRVSVVRPQPGDTGRCINFTR	303
Qy	487	VKNQNPQAKYPLNNAVHTSSPPPAIYTPPPAPhCCEPPPSAPAPPIPSSTLPPPPQA	546
Db	304	VKNQNPQAKYPLNNTYHPSSPPPAIYTPPPAPhCCEPPPSAPAPPIPSSTLPPPPQA	363
Qy	547	PPPPRAPPSPSRPPPSV	564
Db	364	PPPPRAPPSPSRPPPSV	381

QY	DB	Query Match	Best Local Match	Similarity	94.8%	Pred. No. 7.1e-138	Matches 367	Conservative	2	Mismatches 7	Indels 11	Gaps 1
QY	DB	1	MATERRALIGIGFQWL	SLATTVLILCAGGGRREDGSPACVGGFDLYFLIDKSGSVLHHMN	60							
QY	DB	1	MATERRALIGIGFQWL	SLATTVLILCAGGGRREDGSPACVGGFDLYFLIDKSGSVLHHMN	60							
QY	DB	61	EIYYVEEQLAHKEFISPOLRMSFTVSTNGTTLMKLTEDREIQRLGEBELQKVLPGSDTYM	120								
QY	DB	61	EIYYVEEQLAHKEFISPOLRMSFTVSTNGTTLMKLTEDREIQRLGEBELQKVLPGSDTYM	120								
QY	DB	121	HEGFERRASEQIYYENRQGRVTRTSVLIATLDGELHEDLPFYSERENRNSRDGAIYYCVGV	180								
QY	DB	121	HEGFERRASEQIYYENRQGRVTRTSVLIATLDGELHEDLPFYSERENRNSRDGAIYYCVGV	180								
QY	DB	181	KDFNFTOLARINDSKDHYFPVNDGFOALQGIHSHILKSKSCIEIILAAEPSTICAGESFOVY	240								
QY	DB	181	KDFNFTOLARINDSKDHYFPVNDGFOALQGIHSHILKSKSCIEIILAAEPSTICAGESFOVY	240								
QY	DB	241	VRGNQFRHARANDRYLCSFKINDSVTLNEKPPSVEDTYLLCAPILKEVGMKALQVSMN	300								
QY	DB	241	VRGNQFRHARANDRYLCSFKINDSVTLNEKPPSVEDTYLLCAPILKEVGMKALQVSMN	300								
QY	DB	301	DGLSFTSSSVIITTHHCSGSLIATALLIFLLILALALMMFWPLCTVYIKEVPPRAE	360								
QY	DB	301	DGLSFTSSSVIITTHHCSGSLIATALLIFLLILALALMMFWPLCTVYIKEVPPRAE	360								
QY	DB	361	ESEEDDDGLPKKKWPTVDASYGGRG	387								

```
Db          ||||| |  
            :  
361 ESEVSDH$RMA-----VGQC 376  
  
RESULT 11  
US-09-833-245-620  
; Sequence 620, Application US/09833245  
; Publication No. US20040010134A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF546PCT  
; CURRENT APPLICATION NUMBER: US/09/833,245  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229, 358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256, 931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/1199, 384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: Patentin Ver. 2.1
```

QY	1	MATARRALGIGFQWLSTATLVLCAGCGRRREDGSPACGGFDFYFLIDKSGSVLHMNN	60
DB	1	MATARRALGIGFQWLSTATLVLCAGCGRRREDGSPACGGFDFYFLIDKSGSVLHMNN	60
QY	61	EIYYVEQLAKKFTISPOLRMSFIYFSTGTITLMKLTERRDQIRQGLBELQKVLPGSDITVM	120
DB	61	EIYYVEQLAKKFTISPOLRMSFIYFSTGTITLMKLTERRDQIRQGLBELQKVLPGSDITVM	120
QY	121	HEGFERRASEQIYYENRQGYRTASVIALTTDELHEDLFFYSERREANRRSRDICAIVYCVGV	180
DB	121	HEGFERRASEQIYYENRQGYRTASVIALTTDELHEDLFFYSERREANRRSRDICAIVYCVGV	180
QY	181	KDPNETQIARIADSKDHVPVNDGFOALQGIHSHILKSKSCIEILAAEPSTTCAGSPQVY	240
DB	181	KDPNETQIARIADSKDHVPVNDGFOALQGIHSHILKSKSCIEILAAEPSTTCAGSPQVY	240
QY	241	VRGNQFRRARAVDRVLCSFKINDSVTLNEKRPSEVDITLLCPAPILKEVGKAAALQVSMN	300
DB	241	VRGNQFRRARAVDRVLCSFKINDSVTLNEKRPSEVDITLLCPAPILKEVGKAAALQVSMN	300
QY	301	DGLSFISSSVITITTHCGSDGSIILAIALLILFLALALALMLMFWPCLCTVIIKEVPPPAE	360
DB	301	DGLSFISSSVITITTHCGSDGSIILAIALLILFLALALALMLMFWPCLCTVIIKEVPPPAE	360
QY	361	ESSEED 366	
DB	361	ESSEED 366	

```
RESULT 12
US-10-038-307-18
/ Sequence 18, Application US/10038307
/ Publication No. US20030134786A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/038,307
/ CURRENT FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 551
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-038-307-18

Query Match          54.9%; Score 1661; DB 14; Length 551;
Best Local Similarity 100.0%; Pred. No. 1e-119;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATARRALGIGFQWLSLTLVLIICAGCGRRDGGPACYGFDLYFLIDKSGSVLHWN 60
DB 1 MATARRALGIGFQWLSLTLVLIICAGCGRRDGGPACYGFDLYFLIDKSGSVLHWN 60
QY 61 EIVYVEQIAHKFISPOLRMSFIVFSTRTGTTLMKLTREBQIRQGLELOKVLPGDPTM 120
DB 61 EIVYVEQIAHKFISPOLRMSFIVFSTRTGTTLMKLTREBQIRQGLELOKVLPGDPTM 120
QY 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSEERANRSRDGAIVYCVG 180
DB 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSEERANRSRDGAIVYCVG 180
QY 181 KOPNETQIARIADSKDHFVPVNDGFQALQGIHSLIKSCIEIILAEPSTICAGESFOV 240
DB 181 KOPNETQIARIADSKDHFVPVNDGFQALQGIHSLIKSCIEIILAEPSTICAGESFOV 240
QY 241 VRGNFRRARNDVRLCSFKINDSVTLNKPESVEDTYLLCPAPILKEVGMKALQVSMN 300
DB 241 VRGNFRRARNDVRLCSFKINDSVTLNKPESVEDTYLLCPAPILKEVGMKALQVSMN 300
QY 301 DGLSFISSSVITTTTHCSDG 320
DB 301 DGLSFISSSVITTTTHCSDG 320

RESULT 13
US-10-201-292-18
/ Sequence 18, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 551
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-201-292-18

Query Match          54.9%; Score 1661; DB 14; Length 551;
```

```
Best Local Similarity 100.0%; Pred. No. 1e-119;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATARRALGIGFQWLSLTLVLIICAGCGRRDGGPACYGFDLYFLIDKSGSVLHWN 60
DB 1 MATARRALGIGFQWLSLTLVLIICAGCGRRDGGPACYGFDLYFLIDKSGSVLHWN 60
QY 61 EIVYVEQIAHKFISPOLRMSFIVFSTRTGTTLMKLTREBQIRQGLELOKVLPGDPTM 120
DB 61 EIVYVEQIAHKFISPOLRMSFIVFSTRTGTTLMKLTREBQIRQGLELOKVLPGDPTM 120
QY 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSEERANRSRDGAIVYCVG 180
DB 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSEERANRSRDGAIVYCVG 180
QY 181 KOPNETQIARIADSKDHFVPVNDGFQALQGIHSLIKSCIEIILAEPSTICAGESFOV 240
DB 181 KOPNETQIARIADSKDHFVPVNDGFQALQGIHSLIKSCIEIILAEPSTICAGESFOV 240
QY 241 VRGNFRRARNDVRLCSFKINDSVTLNKPESVEDTYLLCPAPILKEVGMKALQVSMN 300
DB 241 VRGNFRRARNDVRLCSFKINDSVTLNKPESVEDTYLLCPAPILKEVGMKALQVSMN 300
QY 301 DGLSFISSSVITTTTHCSDG 320
DB 301 DGLSFISSSVITTTTHCSDG 320

RESULT 14
US-09-796-753-12
/ Sequence 12, Application US/09796753
/ Publication No. US20030027998A1
/ GENERAL INFORMATION:
/ APPLICANT: McCarthy, Sean A.
/ TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
/ FILE REFERENCE: 7853-227-999
/ CURRENT APPLICATION NUMBER: US/09/796,753
/ CURRENT FILING DATE: 2001-03-01
/ PRIOR APPLICATION NUMBER: 09/183,175
/ PRIOR FILING DATE: 1998-10-30
/ PRIOR APPLICATION NUMBER: 09/223,094
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/223,546
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/224,246
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/259,388
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/1122,458
/ PRIOR FILING DATE: 1999-03-01
/ PRIOR APPLICATION NUMBER: 09/312,359
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: 09/336,536
/ PRIOR FILING DATE: 1999-06-18
/ PRIOR APPLICATION NUMBER: 09/342,687
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 09/345,464
/ PRIOR FILING DATE: 1999-06-30
/ PRIOR APPLICATION NUMBER: 09/365,164
/ PRIOR FILING DATE: 1999-07-30
/ PRIOR APPLICATION NUMBER: 09/399,723
/ PRIOR FILING DATE: 1999-09-20
/ PRIOR APPLICATION NUMBER: 09/409,634
/ PRIOR FILING DATE: 1999-09-30
/ PRIOR APPLICATION NUMBER: 09/471,179
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 09/474,071
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/474,072
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/514,010
/ PRIOR FILING DATE: 2000-02-25
/ PRIOR APPLICATION NUMBER: 09/516,745
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 12
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
US-09-796-753-12

Query Match 54.5%; Score 1649; DB 10; Length 333;
Best Local Similarity 100.0%; Pred. No. 4,4e-119;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATARRALGIGFOWLSLTLVLI CAGGGRREDGPGACGFDLYFLIDKSGSVLHHMN 60
DB 1 MATARRALGIGFOWLSLTLVLI CAGGGRREDGPGACGFDLYFLIDKSGSVLHHMN 60
QY 61 EIYFVEQLAHKFISPOLRMSFIVFSTRTTLMKLTEDREOIRQGLELOKVLPGSDTYM 120
DB 61 EIYFVEQLAHKFISPOLRMSFIVFSTRTTLMKLTEDREOIRQGLELOKVLPGSDTYM 120
QY 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVG 180
DB 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVG 180
QY 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCIEIILAEPSSTICAGESFQV 240
DB 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCIEIILAEPSSTICAGESFQV 240
QY 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
DB 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
QY 301 DGLSFSSSVIITTTTCS 318
DB 301 DGLSFSSSVIITTTTCS 318

RESULT 15
US-10-038-307-2
Sequence 2, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FaSTSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-2

Query Match 54.5%; Score 1649; DB 14; Length 333;
Best Local Similarity 100.0%; Pred. No. 4,4e-119;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATARRALGIGFOWLSLTLVLI CAGGGRREDGPGACGFDLYFLIDKSGSVLHHMN 60
DB 1 MATARRALGIGFOWLSLTLVLI CAGGGRREDGPGACGFDLYFLIDKSGSVLHHMN 60
QY 61 EIYFVEQLAHKFISPOLRMSFIVFSTRTTLMKLTEDREOIRQGLELOKVLPGSDTYM 120
DB 61 EIYFVEQLAHKFISPOLRMSFIVFSTRTTLMKLTEDREOIRQGLELOKVLPGSDTYM 120
QY 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVG 180
DB 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVG 180
QY 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCIEIILAEPSSTICAGESFQV 240
DB 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCIEIILAEPSSTICAGESFQV 240
QY 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
DB 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
QY 301 DGLSFSSSVIITTTTCS 318
DB 301 DGLSFSSSVIITTTTCS 318

Search completed: June 21, 2004, 14:02:13
Job time : 57.2859 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 22, 2004, 02:37:46 ; Search time 548.154 Seconds

(without alignment)
3075.489 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914
Sequence: 1 MATERRALGIGFQWLSLAT.....VIEKVPPEPPESEENKIK 368

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delext 7.0	

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO/US0970076/runac_21062004_125533_8805/app_query.fasta_1.2140
-DB=Published Applications NA -QPM=faeap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40 cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pcr -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US0970076_@CGN_1.1.1225_@runac_21062004_125533_8805
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/2/pubpna/US09C_NEW_PUB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1914	100.0	1454	16	US-10-133-937-58	Sequence 58, Appl
2	1914	100.0	1454	16	US-10-159-563-58	Sequence 58, Appl
3	1894	99.0	5540	13	US-09-918-715-176	Sequence 176, App
4	1894	99.0	5540	13	US-09-918-715-231	Sequence 231, App
5	1894	99.0	5540	15	US-10-301-822-198	Sequence 198, App
6	1793	93.7	5220	13	US-09-918-715-186	Sequence 186, App
7	1793	93.7	5220	13	US-09-918-715-300	Sequence 300, App
8	1661	86.8	1674	15	US-10-038-307-17	Sequence 17, Appl
9	1661	86.8	1674	15	US-10-201-292-17	Sequence 17, Appl
10	1650	86.2	1650	15	US-10-038-307-13	Sequence 13, Appl
11	1650	86.2	1650	15	US-10-038-307-15	Sequence 15, Appl
12	1650	86.2	1650	15	US-10-201-292-13	Sequence 13, Appl
13	1650	86.2	1650	15	US-10-201-292-23	Sequence 23, Appl
14	1649	86.2	1056	15	US-10-201-292-23	Sequence 23, Appl
15	1649	86.2	1056	15	US-10-038-307-19	Sequence 19, Appl
16	1649	86.2	1713	15	US-10-201-292-21	Sequence 21, Appl
17	1649	86.2	1713	15	US-09-796-753-11	Sequence 11, Appl
18	1649	86.2	2272	10	US-10-038-307-1	Sequence 1, Appl
19	1649	86.2	2272	15	US-10-201-292-1	Sequence 1, Appl
20	1649	86.2	2352	15	US-10-198-846-9957	Sequence 9957, Ap
21	1649	86.2	2352	15	US-09-833-381-998	Sequence 998, App
22	1649	86.2	2459	9	US-10-038-307-9	Sequence 9, Appl
23	1640	85.7	1650	15	US-10-201-292-9	Sequence 9, Appl
24	1640	85.7	1650	15	US-10-038-307-25	Sequence 25, Appl
25	1636	85.5	1008	15	US-10-201-292-25	Sequence 25, Appl
26	1636	85.5	1008	15	US-10-038-307-21	Sequence 21, Appl
27	1634.5	85.4	1047	15	US-10-201-292-15	Sequence 15, Appl
28	1634.5	85.4	1047	15	US-10-201-292-15	Sequence 15, Appl
29	1548	80.9	1608	15	US-10-062-674-1757	Sequence 1757, Ap
30	1520	79.4	2397	16	US-10-038-307-11	Sequence 11, Appl
31	1509	78.8	1623	15	US-10-201-292-11	Sequence 11, Appl
32	1509	78.8	1623	15	US-10-201-292-33	Sequence 33, Appl
33	1509	78.8	1623	15	US-10-037-270-8	Sequence 8, Appl
34	1492	72.7	1609	15	US-10-117-222-8	Sequence 8, Appl
35	1392	72.7	1609	16	US-10-201-292-31	Sequence 31, Appl
36	1313	66.6	1464	15	US-10-201-292-27	Sequence 27, Appl
37	1193	62.3	1401	15	US-10-104-047-669	Sequence 669, App
38	1193	62.3	1401	15	US-10-368-087-9	Sequence 9, Appl
39	962.5	50.3	4081	15	US-09-796-753-51	Sequence 51, Appl
40	962.5	50.3	4081	15	US-10-038-307-5	Sequence 5, Appl
41	957.5	50.0	3677	15	US-10-201-292-5	Sequence 5, Appl
42	957.5	50.0	3677	15	US-10-038-307-5	Sequence 5, Appl
43	957.5	50.0	3677	15	US-10-201-292-5	Sequence 5, Appl
44	957.5	50.0	4348	10	US-09-814-353-22000	Sequence 22000, A
45	941.5	49.2	5222	15	US-10-006-285-443	Sequence 443, App

ALIGNMENTS

RESULT 1
US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:

Pred. No.: 5,086-239 Length: 1454
 Score: 1914.00 Matches: 368
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 16 Gaps: 0

US-09-970-076-2 (1-368) x US-10-133-937-58 (1-1454)

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Oy      1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db      144 ATGGCCAGCGGAGCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTGGCCCACT 203

Oy      21 LeuValLeuIleCyAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTyr 40
Db      204 CTGGTGCTCATCTGCGCGGCGAGGGGAGCGCAGGAGAGATGGGGGTCCAGCTGCTAC 263

Oy      41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db      264 GCGCGATTTGACCTGTACTTCACTTTTGGACAAATCAGGAAGTGTCTGCACACCTGGAAT 323

Oy      61 GluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
Db      324 GAAATCTATTACTTGTGGAAACAGTTGGCTCCAAATTCATCAGCCCAAGTTGAGAAATG 383

Oy      81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db      384 TCCTTATTGTTTTCCTCAACCGAGGAAACACCTTAATGAACTGACAGAAAGACAGAA 443

Oy      101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db      444 CAAATCCGTCAGAGCCTAGGAAGAACTCCAGAAAGTTGCCAGAGAGAGACACTTACATG 503

Oy      121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
Db      504 CATGAAGATTGTGAAAGGGCCAGTGACAGATTATTTATGAAACAGCAAGAGGATACAG 563

Oy      141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisIleGluAspLeuPhePheTyr 160
Db      564 ACAGCCACGCTCATATGCTTTCCTTAAGTGAAGAACTCCAGAAAGTCTCTTTTCTAT 623

Oy      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db      624 TCAAGAGAGGAGGCTTAATAGTCTCGAATCTGTGCAATGTTTATCTGATGGTGGTGG 683

Oy      181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db      684 AAAGATTTCATGAGACACAGCTGGCCCGGATGGGACAGTAAGGATCATGTGTTTCCC 743

Oy      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db      744 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTAAAGAACTCTGTC 803

Oy      221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
Db      804 ATCGAAATTTTAGAGCGTGAACATCCACCATATGTGCAGAGAGATCATTTCAAGTTGTC 863

Oy      241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db      864 GTGAAGAGAAACGGCTTCCGACATGCCGCAACGTCGACAGGGTCTCTGACGCTTCAAG 923

Oy      261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrThrLeuLeu 280
Db      924 ATCAATGACTGGGTACACTCATATAGAAAGCCCTTTCTGTGGAAGAACCTTATTTACTG 983

Oy      281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db      984 TGTCCAGGCGCATCTTAAAGAAAGTGGCATGAAGTGCACCTCAGCTCAGCATGAAAC 1043

Oy      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
Db      1044 GATGGCCTCTCTTTATCTCCAGTTCTGTCAATCATCACACACACACTGTTCTGACGGT 1103
  
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Oy      321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuTrp 340
Db      1104 TCCATCTGGCCATCGCCCTGCTGATCTGTCTCTGCTCTAGCCCTGGCTCTCTGG 1163

Oy      341 TrpPheTrpProLeuCysCysThrValIleIleIleGluValProProProAlaGlu 360
Db      1164 TGGTTTGGCCCTCTGCTGACATGTATATCAAGAGAGTCCCTCACCCCTGCCGAG 1223

Oy      361 GluSerGluGluLeuLysIleLys 368
Db      1224 GAGAGTAGAGAAATAATAATAA 1247
  
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RESULT 2

US-10-159-563-58

; Sequence 58, Application US/10159563
 ; Publication No. US2004009154A1

GENERAL INFORMATION:

; APPLICANT: Khan, Javed
 ; APPLICANT: Ringner, Markus
 ; APPLICANT: Peterson, Carsten

APPLICANT: Meitzner, Paul

TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR

TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS

FILE REFERENCE: 11613.56US11

CURRENT APPLICATION NUMBER: US/10/159,563

PRIOR FILING DATE: 2002-12-09

PRIOR APPLICATION NUMBER: US 10/133,937

NUMBER OF SEQ ID NOS: 444

SOFTWARE: PatentIn version 3.1

SEQ ID NO 58

LENGTH: 1454

TYPE: DNA

ORGANISM: Homo sapiens

US-10-159-563-58

Alignment Scores:

Pred. No.: 5,086-239 Length: 1454
 Score: 1914.00 Matches: 368
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 16 Gaps: 0

US-09-970-076-2 (1-368) x US-10-159-563-58 (1-1454)

```

Oy      1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db      144 ATGGCCAGCGGAGCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTGGCCACT 203

Oy      21 LeuValLeuIleCyAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTyr 40
Db      204 CTGGTGCTCATCTGCGCGGCGAGGGGAGCGCAGGAGAGATGGGGGTCCAGCTGCTAC 263

Oy      41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db      264 GCGCGATTTGACCTGTACTTTCCTCAACCGAGGAAACCTTAATGAAATCAGACCAAGTGAAGATG 323

Oy      61 GluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
Db      324 GAAATCTATTACTTGTGGAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAATG 383

Oy      81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db      384 TCCTTATTGTTTTCCTCACCGAGGAACAACCTTAATGAAATCAGACAGAAAGACAGAA 443

Oy      101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db      444 CAAATCCGTCAGAGCCTAGGAAGAACTCCAGAAAGTTCGCCAGAGAGACACTTACATG 503

Oy      121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
  
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Db      504 CATGAGGATTTGAAAGGCGCAGTGAGCATTTATATGAAAACAGCAAGAGGTACAGG 563
Qy      141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160
Db      564 ACAGCCACGCTATCATTTGCTTGTGACTGAGTAAGAACTCAGAAAGATCTCTTTTTCAT 623
Qy      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db      624 TCAGAGAGGAGGAGCTAAATGATGCTCGAATCTTGGTCAATTTTCTTACTGCTGTGTGTG 683
Qy      181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db      684 AAAGATTTCAATGAGACACAGCTGGCCGGATTTGGAGACAGTAAGATCATGTGTTTCCC 743
Qy      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db      744 GTGAATGACGGCTTTCAGGCTCTGCAGGACATCATCTCAATTTTGAAGAAAGTCTTCC 803
Qy      221 IleguileleuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
Db      804 ATCGAAATTTTAGACAGCTGACCATTCACATATGTCAGAGAGTCAATTTCAAGTTGTC 863
Qy      241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db      864 GTGAGAGGAAACGGCTTCGACATGCCGCAACGTCGACAGGTCCTCTGCAGCTTCAAG 923
Qy      261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
Db      924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAAGACACTTAATTTACTG 983
Qy      281 CysProAlaProIleLeuLysGluValGlyMetLysValAlaLeuGlnValSerMetAsn 300
Db      984 TGTCACGCGCTATCTTAAAGAAAGTGCATGAAGAGCTGCAGTCCAGTCCAGTGAAC 1043
Qy      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
Db      1044 GATGCCCTCTCTTTATCTCCAGTTCTGTGCATCATCACACACACAGCTTCTGACGCT 1103
Qy      321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuLeuAlaLeuLeuTyr 340
Db      1104 TCCATCTGCGCCATGCCCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1163
Qy      341 ThrPheTrpProLeuCysCysThrValIleIleLysGluValProProProProAlaGlu 360
Db      1164 TGGTCTGCGCCCTCTGCTGCACTGTGATTCAGAGAGTCTCTCCACCCCTGCCGAG 1223
Qy      361 GluSerGluGluAsnLysIleLys 368
Db      1224 GAGACTGAGGAAATTAATAATAAA 1247

RESULT 3
US-09-918-715-176
; Sequence 176, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-09-918-715-176
Alignment Scores:
Pred. No.: 2e-235
Score: 1894.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 98.96%
DB: 13
Gaps: 0

US-09-970-076-2 (1-368) x US-09-918-715-176 (1-5540)
Qy      1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerIleuAlaThr 20
Db      144 ATGGCAGCGGAGAGCGGAGAGCCCTCGGACATCGGCTTCAGTGGCTCTTTGGCCACT 203
Qy      21 LeuValLeuIleCysAlaGlyGlnGlyGlyArgArgGluAspGlyGlyProAlaCysTyr 40
Db      204 CTGGTCTCATCTGGCCGGGCAAGGGGAGGAGGAGGAGATGGGGGTCCAGCCCTGATC 263
Qy      41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db      264 GCGGATTTGACCTGTACTTCAATTTGGACAATCAGAGAGTGTGCTGCACCACTGGAAT 323
Qy      61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
Db      324 GAAATCTATTACTTTGTGAAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 383
Qy      81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db      384 TCTTTATTTGTTTCTCCACCGAGAAACACTTAATGAAGATGACAGAAACAGAGAA 443
Qy      101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db      444 CAAATCCGTCAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCAGAGAGACACTTAACATG 503
Qy      121 HisGluGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
Db      504 CATGAGGATTTGAAAGGCGCAGTGAGCATTTATATGAAAACAGCAAGAGGTACAGG 563
Qy      141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160
Db      564 ACAGCCACGCTATCATTTGCTTGTGACTGAGTAAGAACTCAGAAAGATCTCTTTTTCAT 623
Qy      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db      624 TCAGAGAGGAGGAGCTAAATGATGCTCGAATCTTGGTCAATTTTCTTACTGCTGTGTGTG 683
Qy      181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db      684 AAAGATTTCAATGAGACACAGCTGGCCGGATTTGGAGACAGTAAGATCATGTGTTTCCC 743
Qy      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db      744 GTGAATGACGGCTTTCAGGCTCTGCAGGACATCATCTCAATTTTGAAGAAAGTCTTCC 803
Qy      221 IleguileleuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
Db      804 ATCGAAATTTTAGACAGCTGACCATTCACATATGTCAGAGAGTCAATTTCAAGTTGTC 863
Qy      241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db      864 GTGAGAGGAAACGGCTTCGACATGCCGCAACGTCGACAGGTCCTCTGCAGCTTCAAG 923
Qy      261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
Db      924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAAGAAATTAATTTACTG 983
Qy      281 CysProAlaProIleLeuLysGluValGlyMetLysValAlaLeuGlnValSerMetAsn 300
Db      984 TGTCACGCGCTATCTTAAAGAAAGTGCATGAAGAGTGCAGTCCAGTCCAGTGAAC 1043

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QY	301	ASpGyLyeSeR-PheIleSeRSeRValIleIleThThrThrHisCySeSerAspGly	320
Db	1044	GAAGGCCTCTCTTTATCTCCAGGTTGTGATCATATACACACACACTGTTTGACGGT	110
QY	321	SeRIleLeuAlIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp	340
Db	1104	TCCATCTCGGCATGGCCCTGGCTGATCCGTTCCTGCTCTAGCCCTGGGTCTCCTGG	116
QY	341	TRpPheTrpProLeuCyCySthrValIleIleIleYgluValProProProAlaIglu	360
Db	1164	TGGTTCTGGCCCCCTCTGCTGCACTGTGATTATCAAGAGGTCCCTCACCCCTGCCGAG	122
QY	361	GIuSeRgLuGlu	364
Db	1224	GAGACTGAGGAA	1235
RESULT 4			
US-09-918-715-231			
; Sequence 231, Application US/09918715			
; Publication No. US20030017157A1			
; GENERAL INFORMATION:			
; APPLICANT: Brad St. Croix			
; APPLICANT: Bert Vogelstein			
; APPLICANT: Kenneth Kinzler			
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS			
; FILE REFERENCE: 1107.00134			
; CURRENT APPLICATION NUMBER: US/09/918, 715			
; CURRENT FILING DATE: 2001-08-01			
; PRIOR APPLICATION NUMBER: 60/222, 599			
; PRIOR FILING DATE: 2000-08-02			
; PRIOR APPLICATION NUMBER: 60/224, 360			
; PRIOR FILING DATE: 2000-08-11			
; PRIOR APPLICATION NUMBER: 60/282, 850			
; PRIOR FILING DATE: 2000-04-11			
; NUMBER OF SEQ ID NOS: 358			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 231			
; LENGTH: 5540			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-918-715-231			
Alignment Scores:			
Pred. No.: 2e-235 Length: 5540			
Score: 1894.00 Matches: 364			
Percent Similarity: 100.00% Conservative: 0			
Best local Similarity: 100.00% Mismatches: 0			
Query Match: 98.96% Indels: 0			
DB: 13 Gaps: 0			
US-09-970-076-2 (1-368) x US-09-918-715-231 (1-5540)			
QY	1	MetaIaTruAlAGIuARgARgAlaLeuGlyIleGlyPheGlnTrpLeuSerIleuAlaThr	20
Db	144	ATGGCACAAGCGGAGCGAGAGAGCCCTCGGCATGGCTTCCAGTGGCTCTCTTGGCCACT	203
QY	21	LeuValIleuIleCyAlaIaGlyGlnGlyIaYARgAGluAspGlyIProAlaCyTYr	40
Db	204	CTGGGCTCATCTGCGCCGGGCAAGGGAGCGAGGAGGATGGGGGTCCAGCTGCTAC	263
QY	41	GIyGIyPheAspLeuTYrPheIleLeuAspIySeRgLySeRValIleuHisSTpAn	60
Db	264	GCGCGATTTGACCTGTACTTCAATTTTGGACCAATCGAGAAAGTGTGTGCACCACTGGAAAT	323
QY	61	GIuIeTYrTYrPheValGluGlnLeuAlaHisIlyPheIleSeRProGlnLeuArGmet	80
Db	324	CAAAATCTATTACTTGTGTGAACAGTTGGCTCACAAATTCATTCAGCCCAAGTTGAAGATG	383
QY	81	SeRpheIleValPheSeRThARgGIyThrThrLeuMetIySeRThARgIuAspARgIu	100
Db	384	TGCTTTATTGTTTCTCCACCGAGGACAACACTTATGAAATGTGACAGAGACAGAGA	443
QY	101	GInIleARgGInGlyLeuGlnGluLeuGlnIlySeValIleuProGlyGlyAspThrTYrmet	120

Db	444	CAATTCGCTCAGGCGCTTGAAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG	503
Qy	121	HisgluGlyPhegluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg	140
Db	504	CATGAAGGATTTGAAAGGGCCAGGACAGATTTATTATGAAAAACAACAAGGGTACAGG	563
Qy	141	ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisgluAsnLeuPhePheTyr	160
Db	564	ACACCACGCGTCATCATGCTTGTGACTGATGAGAAATCCCATGAAAGATCTTTTTCAT	623
Qy	161	SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal	180
Db	624	TCAAGAGGGAGGCTAATAGGTCTCCAGATCTTGTCATATGTTACTGTGTTGGTGTG	683
Qy	181	LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro	200
Db	684	AAAGATTTCAATGAGACACAGCTGGCCCGGATTTGCCGACGTAAAGATCATGTGTTCCC	743
Qy	201	ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuGlySerCys	220
Db	744	GTAATACAGGCTTTCAGGCTCTGGCAAGGACATCATCACTCAATTTTGAAGAACTCTGC	803
Qy	221	IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal	240
Db	804	ATCGAAATTTCTAGACGTGAACCATCCACATATGTCCAGAGAGTCAATTTCAAGTTGTC	863
Qy	241	ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys	260
Db	864	GTGAGAGGAAACGGCTTCCGACATGCCCGCACTGGACAGAGGCTCTGTGACGCTTCAAG	923
Qy	261	IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu	280
Db	924	ATCATATGACTCGGTCACACTCAAGAGAAAGCCCTTTCTGTGAAAGATCACTTATTTACTG	983
Qy	281	CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn	300
Db	984	TGTCACGCGCTTATCTTAAAGAGAGTTGGCATGAAGCTGCATCCAGGTCAGCATGAC	1043
Qy	301	AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrHisCysSerAspGly	320
Db	1044	GATGGCCCTCTTTTATCTCCAGTCTGTCAATCATCAACACACACTGTGTTGACGGT	1103
Qy	321	SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuLeuAlaLeuLeuTyr	340
Db	1104	TCCATCTCTGGCAATCGCCCTGTGATCTGTCTCTGCTGCTGAGCCCTGCTCTCTCTGG	1163
Qy	341	TrpPheTrpProLeuCysCysThrValIleIleLysGluValProProProAlaGlu	360
Db	1164	TGTTTCTGGCCCCCTCTGCTGCACTGATATATACAGAGGTTCTCCACCCCTTCCGAG	1223
Qy	361	GluSerGluGlu 364	
Db	1224	GAGAGTGAGGAA 1235	
RESULT 5			
US-10-301-822-198			
; Sequence 198, Application US/10301822			
; Publication No. US20030148410A1			
GENERAL INFORMATION:			
; APPLICANT: Millennium Pharmaceuticals, Inc.			
; APPLICANT: Berger, Allison			
; APPLICANT: Guillemette, Tracy L.			
; APPLICANT: Kamatkar, Shubhangi			
; APPLICANT: Schlegel, Robert			
; APPLICANT: Monahan, John E.			
; APPLICANT: Thibodeau, Stephen N.			
; APPLICANT: BURGART, Lawrence J.			
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND			
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND			
; TITLE OF INVENTION: THERAPY OF COLON CANCER			
; FILE REFERENCE: MEM01-029P2RNM			
; CURRENT APPLICATION NUMBER: US/10/301,822			

```
/ CURRENT FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 60/339,971
/ PRIOR FILING DATE: 2001-12-10
/ PRIOR APPLICATION NUMBER: US 60/361,978
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/381,988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: PaetSeq for Windows Version 4.0
/ SEQ ID NO 198
/ LENGTH: 5540
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (144)...(1838)
/ US-10-301-822-198

Alignment Scores:
Pred. No.: 26-235      Length: 5540
Score: 1894.00      Matches: 364
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 98.96%      Indels: 0
DB: 15      Gaps: 0

US-09-970-076-2 (1-368) x US-10-301-822-198 (1-5540)

QY 1 MetAlArhAlaGluAArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCAGCGGGGAGGAGGAGAGCCCTGGCATCGGCTTCACATGGCTCTTTGGCCACT 203
QY 21 LeuValLeuIleCyAaIaGlyGlnGlyAArgAArgIuAArgGlyProAlaCyA 40
DB 204 CTGGGTCTCATCTGGCCCGGCAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 263
QY 41 GlyGlyPheAArgLeuTrpPheIleLeuAArgIuSerValLeuHisIleTrpAn 60
DB 264 GCGGAGTTTGACCTGATCTTCACTTTCACAAATCGAAGAGTGCTGCACACCTGGAA 323
QY 61 GluIleTyTrpPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuAArg 80
DB 324 GAAATCTATTAATTTGTGGACAGTTGGCTCAAAATTCATGACGCCACAGTTGAAGAT 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLeuLeuThrGluAArgGlu 100
DB 384 TCCCTTATGTTTCTCCACCCGAGGAGCAACCTTAATGAATGACAGAAACAGAGA 443
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnValLeuProGlyIuAAspThrTyMet 120
DB 444 CAAATCCGTCAGAGGCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGAGACCTTACATG 503
QY 121 HisGlnGlyPheGluAArgAlaSerGlnGlnIleTyTrpGluAAspAArgGlnGly 140
DB 504 CATGAAGATTGAAAGGCGCCAGTAGACAGATTATTAAGAAACAGAAAGGATCAGG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrAArgGlyGluLeuHisGluAArgLeuPhe 160
DB 564 ACAGCCAGCGTCATCATTTCTTGACTGATGAGAGAACTCATGAGAGATCTCTTTTCTAT 623
QY 161 SerGluAArgGluAAspAArgSerAArgLeuGluValAlaIleValTyCyAaIaGly 180
DB 624 TCAGAGAGGAGGAGGCTAATAGTCTCAGAGTCTTGGCAATGTTTACTGTGTGGTGG 683
QY 181 LysAAspPheAAspGluThrGlnLeuAlaArgIleAlaAAspSerLysAAspHisValPhePro 200
DB 684 AAAGATTTCATGAGACACACAGCTGCGCCGAGTTGCGGACAGTAAGATCATGTGTTCC 743
QY 201 ValAAspAArgGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCyA 220
DB 744 GTGAATGACGCGCTTCAGGCTCTGCAAGGACATCATCAATTTTGAAGAGCTTCG 803
QY 221 IleguIleLeuAlaIleGluProSerThrIleCyAaIaGlyGluSerPheGlnVal 240
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DB 804 ATCGAAATTCAGACGCTGAACCATCCACATATGTGACGAGAGCTCATTTCAATTGTC 863
QY 241 ValAArgGlyAAspGlyPheAArgHisAlaAArgAAspAArgValLeuCySerPheLys 260
DB 864 GTGAAGAGGAAACGCGCTTCGACATCCCGCAACGTCGACAGGCTCTCTGACGCTTCAAG 923
QY 261 IleAAspAArgSerValThrLeuAAspGluLysProPheSerValGluAAspThrTyTrpLeu 280
DB 924 ATCAATGACCTGCTACACTCAATAGAGAGCCCTTCTGTGAGAGATATTATTACTG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAAsn 300
DB 984 TCTCCAGCGCCCTATTTTAAAGAACTTGGCATGAAGCTGACCTCAGTCAAGTCAAG 1043
QY 301 AAspGlyLeuSerPheIleSerSerValIleIleThrThrHisCySerAAspGly 320
DB 1044 GATGCGCTCTCTTTTATCTCCAGTTCTGTGCATCATCACACACACACACTGTTCTGACG 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
DB 1104 TCCATCTGCGCCATGCGCTGCTGATCTGTTCTGCTCTAGCCCTGCTCTCTG 1163
QY 341 TrpPheTrpProLeuCyAaIeThrValIleIleLysGluValProProProAlaGlu 360
DB 1164 TCGTCTGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
QY 361 GluSerGlnGlu 364
DB 1224 GAGAGTGAGAA 1235
```

```
RESULT 6
US-09-918-715-186
/ Sequence 186, Application US/09918715
/ Publication No. US20030017157A1
/ GENERAL INFORMATION:
/ APPLICANT: Brad St. Croix
/ APPLICANT: Bert Vogelstein
/ APPLICANT: Kenneth Kinzler
/ TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
/ FILE REFERENCE: 1107.00134
/ CURRENT APPLICATION NUMBER: US/09/918,715
/ CURRENT FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/222,599
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 60/224,360
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: 60/282,850
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 358
/ SOFTWARE: PaetSeq for Windows Version 3.0
/ SEQ ID NO 186
/ LENGTH: 5220
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ US-09-918-715-186

Alignment Scores:
Pred. No.: 2,836-222      Length: 5220
Score: 1793.00      Matches: 342
Percent Similarity: 97.75%      Conservative: 6
Best Local Similarity: 96.07%      Mismatches: 8
Query Match: 93.68%      Indels: 0
DB: 13      Gaps: 0

US-09-970-076-2 (1-368) x US-09-918-715-186 (1-5220)

QY 9 LeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThrLeuValLeuIleCyAaIaGlyGln 28
DB 232 CTGGGTGCGGCGGCGGAGACTGCGTGGCTGACCTGCTGCTGCTGCTGCTGCTGCGGAGAC 351
QY 29 GlyGlyAArgAArgGluAAspGlyGlyProAlaCyAArgIuAArgLeuTrpPheIle 48
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Qy 229 SerThiIleCyAlaGlyGlySerPheGlnValIValArgIYAsnGlyPheArgHis 248
Db 952 TTCACCATCTGCGCGGAGAGTCTTTCAAGTGTGTGTAAGAGAAATGGCTTCGACAT 1011
Qy 249 AlaArgAsnValAspArgValIleuCySerPheIleAsnAspSerValThrIleuAsn 268
Db 1012 GCCCGCAATGTGGACAGGGTCTCTGACACTTCAAAATCAATGACTCACTGACGCTCAAT 1071
Qy 269 GlyIlePhePheSerValIleuAspThrIleuIleuCyPheProIleuIleuGly 288
Db 1072 GAGAGAGCCCTTGTGTGGAGACACTTATTGTCTGTGCCAGACCAATCTTGAAAGAA 1131
Qy 289 ValIGlyMetIleAlaIleuGlnValIleuSerMetAsnAspGlyIleuSerPheIleSerSer 308
Db 1132 GTTGGCATAAAGCTGCTGACCTGACAGTCAATGACAGGCTGTCTTCACTTCCACT 1191
Qy 309 SerValIleIleThrThrThrIleuCySerAspGlySerIleuValIleuIleu 328
Db 1192 TCTGTATCATCAACCAACACACACTGTTCAAGCGCTTCATCTGCGATTGCTGTG 1251
Qy 329 IleuPheIleuIleuValIleuIleuIleuIleuIleuIleuIleuIleuIleu 348
Db 1252 GTCTCTCTCTGCTGTGCGCTGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1311
Qy 349 ValIleIleIleGlyValIleuProIleuProIleuGlyGlyGly 364
Db 1312 GTGATCATCAAGAGGTCCCTCCACCCCTGTGGAGAGTGAAGAA 1359

RESULT 8
US-10-038-307-17
; Sequence 17, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-17

Alignment Scores:
Pred. No.: 7,246-206 Length: 1674
Score: 1661.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Rec Local Similarity: 100.00% Mismatches: 0
Query Match: 86,784 Indels: 0
DB: 15 Gaps: 0

US-09-970-076-2 (1-368) x US-10-038-307-17 (1-1674)
Qy 1 MetAlaThrAlaGlyArgArgAlaLeuGlyIleGlyPheGlnThrIleuSerIleuAlaThr 20
Db 13 ATGGCCACGCGGAGGCGGAGAGCCCTCGGCACTGCGCTTCAAGTGTCTCTTGGGCCACT 72
Qy 21 LeuValIleuIleCyAlaIleuGlnGlyIleuArgArgIleuAspGlyIleuProIleuIleu 40
Db 73 CTGGTCTCATCTGCGCGGCAAGGCGGAGCGGAGGAGATGGGGGTCCAGCTCTGAC 132
Qy 41 GlyIlePheAspIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 60
Db 133 GGGGAGTTTGAACCTGACTTCACTTGTGACAAATGAGAAAGTGTGTGACCACTGGAAAT 192
Qy 61 GluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 80

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Db 193 GAAATCTATTACTTTGTGGACAGTTGGCTCAAAATTCATCAGCCCACTGTGAAATG 252
Qy 81 SerPheIleValPheSerThrArgIleuIleuIleuIleuIleuIleuIleuIleuIleu 100
Db 253 TCTTTATTGTTTCTTCCACCGAGAGAACACTTAAATGAATCAACAGAAACAGAGAA 312
Qy 101 GlnIleArgGlnGlyIleuGlnIleuGlnIleuIleuValIleuProIleuIleuIleuIleu 120
Db 313 CAATTCCTGCAAGGCTTGAAGAACTCCAGAAAGTCTCCAGAGAGAGACCTTAACAG 372
Qy 121 HisGlnGlyPheGlyArgAlaSerGlnIleuIleuIleuIleuIleuIleuIleuIleu 140
Db 373 CATGAAGATTGAAAGGCGCAGTGAAGATTTATTATGAAGAAACAGCAAGGTACAGG 432
Qy 141 ThrAlaSerValIleIleIleIleuThrAspGlyIleuIleuIleuIleuIleuIleuIleu 160
Db 433 ACAGCAGCGCTATATTGCTTGTGCTGATGAGAACTCCAGAAAGATCTCTTTTCTAT 492
Qy 161 SerGlyArgGlyAlaAsnArgSerArgAspLeuGlyAlaIleValIleuIleuIleuIleu 180
Db 493 TCAAGAGGAGGAGCTAAATAGCTTCAAGATCTTGTGCAATGTTTACTGTGTGTG 552
Qy 181 IysAspPheAsnGlyThrGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 200
Db 553 AAAGATTTCATGAGACACAGCTGCGCGGATTGCGGACAGTAAGATCATGTGTTCC 612
Qy 201 ValAsnAspGlyPheGlnAlaIleuGlnIleuIleuIleuIleuIleuIleuIleuIleu 220
Db 613 GTGAATGACGGCTTCAAGCTCTGCAAGCATCATCCATCAATTTGAAAGATCTCC 672
Qy 221 IleGlyIleuValAlaGlyProSerThrIleuCyAlaGlyGlySerPheGlnValIleu 240
Db 673 ATCGAAATTTGACAGCTGACCACTCACCATATGTGACAGAGATCATTTCAAGTGTG 732
Qy 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValIleuCySerPheIleu 260
Db 733 GTGAGAGGAAAGCGCTTCGACATCCGCAAGTGAAGAGGTCCTGTGACGTTCAAG 792
Qy 261 IleAsnAspSerValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 280
Db 793 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGATATTTTACTG 852
Qy 281 CysProIleuIleuIleuGlyValIleuIleuIleuIleuIleuIleuIleuIleuIleu 300
Db 853 TGTCCAGGCTCTTTATCTTAAAGAGTTGGCATGAAGCTGCACTGCACTGCACTGCA 912
Qy 301 AspGlyLeuSerPheIleuSerSerValIleuIleuIleuIleuIleuIleuIleuIleu 320
Db 913 GATGCGCTCTTTTATCTCCAGTTCTGTGATCATCACACCACTGTTCTGACGCT 972

RESULT 9
US-10-201-292-17
; Sequence 17, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-17

Alignment Scores:
Pred. No.: 7,246-206 Length: 1674

```

Score:	1661.00	Matches:	320
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	86.78%	Indels:	
DB:	15	Gaps:	0

US-09-970-076-2 (1-368) x US-10-201-292-17 (1-1674)

Qy	1	MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnIleThrPheSerLeuAlaThr	20
Db	13	ATGGCCACGGCGAGGAGAGAGGCCCTTCGGCAGTCGGCTTCAGTGGCTCTTTGGCCACT	72
Qy	21	LeuValLeuIleCysAlaGlyGlnGlyIaArgArgIuaAspGlyGlyProAlaCysTyr	40
Db	73	CTGGTGTCTATCTGGCCCGGGCAGAGGGGAGCCAGAGGAGATGGGGGTCCAGCTGTCTAC	132
Qy	41	GlyGlyPheAspLeuTyrPheIleLeuAspIleSerGlySerValLeuHisIleTrpAsn	60
Db	133	GGGGGATTTGACCTGTACTTTCATTGTCGCAAAATCAGAAAGTGCTGTCACACCTGGAAAT	192
Qy	61	GluIleTyrTyrPheValGluGlnLeuAlaHisIleValPheIleSerProGlnLeuArgMet	80
Db	193	GAATCTATTACTTTGTGGACAGTTGGCTCCAAATTCATCAGCCACACTGATGAATG	252
Qy	81	SerPheIleValPheSerThrArgGlyThrThrLeuMetCysLeuThrGluAspArgGlu	100
Db	253	TCTCTTATGTCTTCTCCACCGAGGAAACAACCTTATGAAATCTGACAGAAAGACAGAA	312
Qy	101	GlnIleArgGlnGlyLeuGluGlnLeuGlnIleValLeuProGlyGlyAspThrTyrMet	120
Db	313	CAAAATCGTCAGAGCCCTTGAAGAAATCCAGAAAGTTCGACAGAGGAGCACTTAATG	372
Qy	121	HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg	140
Db	373	CATGAGAGATTTGAAAAGGCGCAGTGGACGAGATTTTATGAAAACAGACAGGTATACG	432
Qy	141	ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheTyr	160
Db	433	ACAGCCAGCGTCATCATTTGCTTGAATGATGAGAAATCCATGAAGATCTTTTCTCAT	492
Qy	161	SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal	180
Db	493	TCAGAGAGGAGGCTAATAGTCTCCAGATCTTGGTGCAAATGTTTACTGTGGTGAGTG	552
Qy	181	LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro	200
Db	553	AAAGATTTCAATAGACACAGCTGGCCCGGATTCGGGACAGTAAGATCANTGTCTTCCC	612
Qy	201	ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuGlyLysSerCys	220
Db	613	GTGAATACGGCTTTCAAGCTCTGCAGAGCATCATCCACTCAATTTTGAAGAATCTCTGC	672
Qy	221	IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGlySerPheGlnValVal	240
Db	673	ATCGAAATTTTACACACTGAAACCTCCACCAATATGTGACGAGGATCTATTTCAAGTGTG	732
Qy	241	ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys	260
Db	733	GTGAGAGGAAACGGCTTCCGACATGCCCGGCACTGGACAGGGGTCTCTGCAGCTTCAAG	792
Qy	261	IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu	280
Db	793	ATCATATGACTCGGTCACTCAATATGAAGCCCTTTCTGTGGAAAGATCTTATTTACTG	852
Qy	281	CysProAlaProIleLeuLysGlyValAlaGlyMetLysAlaAlaLeuGlnValSerMetAsn	300
Db	853	TGTCCACGGCTATCTTAAAGAAAGTTGGCAATGAAGATGCATCCAGGTGACATGAC	912
Qy	301	AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly	320
Db	913	GATGGCTCTCTTTTATCTCCAGTTGTGTCAATCATCACACACACACTGTGTTGACGGT	972

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US-10-038-307-13
? Sequence 13, Application US/10038307
? Publication NO. US20030134786A1
? GENERAL INFORMATION:
? APPLICANT: James B. ROTTMAN
? APPLICANT: Theresa L. O'KEEFE
? APPLICANT: Engin OZKAYNIAK
? APPLICANT: Judith J. HEALEY
? TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
? FILE REFERENCE: 7853-253-999
? CURRENT APPLICATION NUMBER: US/10/038.307
? CURRENT FILING DATE: 2002-06-28
? NUMBER OF SEQ ID NOS: 26
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 13
? LENGTH: 1650
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-038-307-13

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US-09-970-076-2 (1-368) X US-10-038-307-13 (1-1650)

QY	1	MeAlaThrAlaGlnuArguArgAlaLeuGlyIleGlyPheGlnTPRLeuSerLeuAlaThr	20
Db	1	ATGGCCACGGCGGAGGGAGAGACCCCTGGGCAATGGGCTTCCAGTGAGCTCTCTTTGGCACT	60
QY	21	LeuValLeuIleCysAlaGlyGlnGlyGlyArgArgGluAspGlyGlyProAlaCysTyr	40
Db	61	CTGGTGTCTATCTGGCCCGGGGCAAGGGGGAGCGCAAGAGGATGGGGGGTCCAGCTGTAC	120
QY	41	GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisITPrAsn	60
Db	121	GGGGATTGACCTGTACTTCCATTTTGGCAAAATCAGAAATGTGGCTGCACACTGGAAAT	180
QY	61	GlnIleTyrTyrPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet	80
Db	181	GAATCTATTACTTTGTGGACAGTTGGCTCCAAATTCACTCAGCCCACTTGGAAATG	240
QY	81	SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu	100
Db	241	TCTTTATTATTGTTTCCACCCGAGGAACAACCTTAAGAACTGACAGAGAGACAGAA	300
QY	101	GlnIleArgGlnGlyLeuGlnGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMet	120
Db	301	CAATCCGCTCAAGGCTTGAAGAACTCCAGAAAGTTCTCCAGAGAGAGACACTTAACATG	360
QY	121	HisGlnGlyPheGlnuArgAlaSerGlnGlnIleTyrTyrGluAspArgGlnGlyTyrArg	140
Db	361	CATGAAGATTTGAAGGGCCAGTACAGCATTTTATTGAAAACAGCAAGGGTACAGG	420
QY	141	ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGlyAspLeuPheTyr	160
Db	421	ACAGCCAGCTCACTCATTTGCTTTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT	480
QY	161	SerGlnuArgGlnuLysAspSerArgAspLeuGlyAlaIleValTyrCysValGlyVal	180
Db	481	TCAGAGGGAGGCTAAATAGTCTCGAAGATCTTGGCAATTTGTTACTGTGGTGGTG	540
QY	181	LysAspPheAsnGlnuThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro	200
Db	541	AAAGATTTCAATGAGCACACGCTGGCCCGGAGATTGGGACACATGAAGATCATGTGTTCCC	600
QY	201	ValAspAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys	220
Db	601	GTAATGACCGGCTTTACGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAACTCTGCG	660

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QY 221 IlegiulleuAlaAgluproserThriIeCyAlaAglyGlySerPheGlnVal 240
DB 661 ATCGAAATTTCTGACGCTGACACCTGACCATATGTCAGAGAGTCAATTTCAAGTTGTC 720
QY 241 ValArgGlyAanglyPheArgHisAlaArgaenValAsparGlyValLeuCySerPheLys 260
DB 721 GTGAGAGGAAACGGCTTCGACATGCGCGCAACGTGAGAGGCTCTGTCGACGTTCAAG 780
QY 261 IleAnaSerSerValThriLeuAanglyLysPhePheSerSerValGlnAspThrTyrlLeu 280
DB 781 ATCAATGACTCGGTCACTCAATGAGAGCCCTTTCTGTGAGAGATCTATTTACTG 840
QY 281 CysProAlaProIleLeuLysGlyValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 841 TGTCCAGCGCTTATCTTAAAGAGTGGCATGAAGGTCAGCTCAGGTCAGATGAAC 900
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThriIeCySerAspGly 320
DB 901 GATGGCTCTCTTTATCTCCAGTTCTGTGCATCATCACACACACACTGTTCTCCCAA 960
QY 321 Ser 321
DB 961 TCT 963

RESULT 11
; Sequence 15, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-15

Alignment Scores:
Pred. No.: 1,936-204 Length: 1650
Score: 1650.00 Matches: 319
Percent Similarity: 99.38% Conservative: 0
Best Local Similarity: 99.38% Mismatches: 2
Query Match: 86.21% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-2 (1-366) x US-10-038-307-15 (1-1650)
QY 1 MetAlaThrAlaGlyArgArgAlaLeuGlyIleGlyPheGlnThrLeuSerLeuAlaThr 20
DB 1 ATGGCCAGCGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 60
QY 21 LeuValIleuIleCyAlaGlyGlnGlyArgArgGlyValAspGlyGlyProIleAspGly 40
DB 61 CTGGGCTCATCTGCGCGCGGCAAGGGGACCGCAGGAGAGAGTGGGGCTCCAGCTGCTAC 120
QY 41 GlyGlyPheAspLeuTyrlPheIleLeuAspLysSerGlySerValLeuHisIleThrAsn 60
DB 121 GCGGGAATTTGACCTGACTTCTTTGGACAAATCAGAAAGTGTCTGACACACCTGGAA 180
QY 61 GlyIleTyrlTyrlPheValGlnGlnLeuAlaHisIlyPheIleSerProGlnLeuArgMet 80
DB 181 GAAATCTATTACTTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 240
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlnAspArgGln 100

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DB 241 TCTTTATTTGTTTCTCCACCGAGAACACTTAATGAACCTGACAGAGACAGAGA 300
QY 101 GlnIleArgGlnGlyLeuGlnGlyLeuGlnLysValIleuProGlyValAspThrTyrlMet 120
DB 301 CAATCCCTCAAGGCTTGAAGAACTCCAGAAAGTTCTCGCAGGAGAGACCTTAACATG 360
QY 121 HisGlyGlyPheGlyArgAlaSerGlyGlnIleTyrlTyrlGlyLysAsnArgGlnIlyTyrlArg 140
DB 361 CATGAAGATTTGAAGAGGCGCAGTGAAGATTTATTTGAAAACAGACAGGATACAG 420
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGlyAspLeuPheMetTyrl 160
DB 421 ACAGCCAGCTCATATTTGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 480
QY 161 SerGlyArgGlyAlaAsnArgSerArgAspLeuGlyAlaIleValTyrlCyValGlyVal 180
DB 481 TCAGAGAGGAGGCTTAATAGGCTTCGAGATCTGTGCAATTTGTTACTGTGTGTGTG 540
QY 181 LysAspPheAanglyThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 541 AAAGATTCAATGAGACACAGCTGCGCGAGTGGCAACAGTGAAGATCATGTGTTCCC 600
QY 201 ValAnaSerGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
DB 601 GTGAATGACGCTTTCAGGCTTCGACAGCATCATCCACTCAATTTGAAGAAGCTCTGC 660
QY 221 IlegiulleuAlaAgluproserThriIeCyAlaAglyGlySerPheGlnVal 240
DB 661 ATCGAAATTTCTGACGCTGACACCTGACCATATGTCAGAGAGTCAATTTCAAGTTGTC 720
QY 241 ValArgGlyAanglyPheArgHisAlaArgaenValAsparGlyValLeuCySerPheLys 260
DB 721 GTGAGAGGAAACGGCTTCGACATGCGCGCAACGTGAGAGGCTCTGCGACTTCAG 780
QY 261 IleAnaSerSerValThriLeuAanglyLysPhePheSerSerValGlnAspThrTyrlLeu 280
DB 781 ATCAATGACTCGGTCACTCAATGAGAGCCCTTTCTGTGAGAGATCTATTTACTG 840
QY 281 CysProAlaProIleLeuLysGlyValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 841 TGTCCAGCGCTTATCTTAAAGAGTGGCATGAAGTGCATCAGGTCAGATGAAC 900
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThriIeCySerAspGly 320
DB 901 GATGGCTCTCTTTATCTCCAGTTCTGTGCATCATCACACACACACTGTTCTCCCAA 960
QY 321 Ser 321
DB 961 TCT 963

RESULT 12
US-10-201-292-13
; Sequence 13, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-13

Alignment Scores:

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Pred. No.: 1,93e-204 Length: 1650
 Score: 1650.00 Matches: 319
 Percent Similarity: 99.38% Conservative: 0
 Best Local Similarity: 99.38% Mismatches: 2
 Query Match: 86.21% Indels: 0
 DB: 15 Gaps: 0

US-09-970-076-2 (1-368) x US-10-201-292-13 (1-1650)

Qy 1 MetAlaThrAlaGluArgAlaLeuGlyTlleGlyPheGlnTrpLeuSerLeuAlaThr 20
 Db 1 ATGGCCAGCGGAGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 60
 Qy 21 LeuValLeuIleCyAlaGlyGlnGlyAlaArgArgGluAspGlyGlyProAlaCysTyr 40
 Db 61 CTGGGCTCATCTGGCGGGGCGAAGGGGAGCGAGGAGGAGTGGGGGTCCAGGCTGCAC 120
 Qy 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
 Db 121 GCGCGATTGACCTGACTTCTCATTTTGGCAAAATCAGAAAGTGTGCTCACACTGGAAAT 180
 Qy 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
 Db 181 GAAATCTATTACTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 240
 Qy 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
 Db 241 TCCCTTATTGTTTCTCCACCGAGGAAACAACCTTAAGAAATCAGAAAGACAGAGAA 300
 Qy 101 GlnIleArgGlnGlyLeuGlnGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
 Db 301 CAAATCCCTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
 Qy 121 HisGlnGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAspArgGlnGlyTyrArg 140
 Db 361 CATGAGGATTTGAAGGGCCAGTAGAGATTTATTAAGAAACAGAAAGGAGACAGG 420
 Qy 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAspLeuPhePheTyr 160
 Db 421 ACAGCCAGCGTCATCATTTGCTTGACTGATGAGAACTCCATGAAAGATCTCTTTTTCAT 480
 Qy 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
 Db 481 TCAGAGAGGAGGCTTAATAGCTCTGAGATCTTGGCAATTTGTTACTGTGTGGTGTG 540
 Qy 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
 Db 541 AAAGATTTCAATGACACAGCTGGCCGAGATTGCGACAGAGATGATGATGTTTCCC 600
 Qy 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
 Db 601 GTGATGACGGGCTTCAAGCTCTGCAAGGCATCACTCATTTTGAAGAAGCCCTGC 660
 Qy 221 IleGluIleLeuAlaIleGluProSerThrIleCysValGlyGlySerPheGlnVal 240
 Db 661 ATCCGAATTTAGACAGCTGAACCATCCACATATGTGACGAGAGTCACTTCAAGTTGTC 720
 Qy 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
 Db 721 GTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGGCTCTGCAAGCTTCAAG 780
 Qy 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
 Db 781 ATCATGACTCGGCTCACACTCAATGAGAAAGCCCTTTCTGTGGAAAGATCTTATTAATG 840
 Qy 281 CysProAlaProIleLeuLysGlyValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
 Db 841 TGTCCAGCGGCTTATCTTAAGAAAGTTGGCATGAAGCTGCAGCTCAGCATGAGAAC 900
 Qy 301 AspGlyLeuSerPheIleSerSerValIleIleThrThrHisCysSerAspGly 320
 Db 901 GATGGCTCTCTTATCTCCAGTTCTGTGCATCATCACCAACCACTGTTCTCCAAA 960

Qy 321 Ser 321
 Db 961 TCT 963

RESULT 13

US-10-201-292-15

; Sequence 15, Application US/10201292
 ; Publication No. US20030144193A1
 ; GENERAL INFORMATION:
 ; APPLICANT: James B. ROTTMAN
 ; APPLICANT: Theresa L. O'KEEFE
 ; APPLICANT: Emgin OZAKYANK
 ; APPLICANT: Judith J. HEALEY
 ; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
 ; FILE REFERENCE: 7853-253-999
 ; CURRENT APPLICATION NUMBER: US/10/201,292
 ; CURRENT FILING DATE: 2003-02-14
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 1650
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-201-292-15

Alignment Scores:

Pred. No.: 1,93e-204 Length: 1650
 Score: 1650.00 Matches: 319
 Percent Similarity: 99.38% Conservative: 0
 Best Local Similarity: 99.38% Mismatches: 2
 Query Match: 86.21% Indels: 0
 DB: 15 Gaps: 0

US-09-970-076-2 (1-368) x US-10-201-292-15 (1-1650)

Qy 1 MetAlaThrAlaGluArgAlaLeuGlyTlleGlyPheGlnTrpLeuSerLeuAlaThr 20
 Db 1 ATGGCCAGCGGAGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 60
 Qy 21 LeuValLeuIleCyAlaGlyGlnGlyAlaArgArgGluAspGlyGlyProAlaCysTyr 40
 Db 61 CTGGGCTCATCTGGCGGGGCGAAGGGGAGCGAGGAGGAGTGGGGGTCCAGGCTGCAC 120
 Qy 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
 Db 61 CTGGGCTCATCTGGCGGGGCGAAGGGGAGCGAGGAGGAGTGGGGGTCCAGGCTGCAC 120
 Qy 61 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
 Db 121 GCGCGATTGACCTGACTTCTTATTTGGCAAAATCAGAAAGTGTGCTCACACTGGAAAT 180
 Qy 121 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
 Db 181 GAAATCTATTACTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 240
 Qy 181 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
 Db 241 TCCCTTATTGTTTCTCCACCGAGGAAACAACCTTAAGAAATCAGAAAGACAGAGAA 300
 Qy 241 GlnIleArgGlnGlyLeuGlnGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
 Db 301 CAAATCCCTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
 Qy 301 HisGlnGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
 Db 361 CATGAGGATTTGAAGGGCCAGTAGAGATTTATTAAGAAACAGAAAGGCTGACAGG 420
 Qy 421 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAspLeuPhePheTyr 160
 Db 421 ACAGCCAGCGTCATCATTTGCTTGACTGATGAGAACTCCATGAAAGATCTTTTTCAT 480
 Qy 481 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
 Db 481 TCAGAGAGGAGGCTTAATAGCTCTGAGATCTTGGCAATTTGTTACTGTGTGGTGTG 540
 Qy 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200

Db 541 AAGATTTCATAGACACAGCTGCCCGATTCGGACAGTAAGATCATGTGTTCCC 600
Qy 201 ValaenaspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValysSerCys 220
Db 601 GTGAATGACGGCTTTCAGGCTCTGCAAGCATCATCTCAATTTTGAAGAAGTCTGC 660
Qy 221 IleguileleuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
Db 661 ATCGAATTTCTAGACAGCTGAACCATTCACATATGTCAGAGAGATCATTTCAAGTTGTC 720
Qy 241 ValaArgGlyAsnGlyPheArgHisAlaIleArgAsnValAspArgValLeuCysSerPheIys 260
Db 721 GTGAGAGGAAACGGCTTCGACATGCTCCGCAACGTGACAGGGCTCTTCGACGTTCAAG 780
Qy 261 IleAsnAspSerValThrIleuAsnGlyuysPropheSerValGluAspThrIleuLeu 280
Db 781 ATCAATGACTCGGTCACTCAATGAGAGCCCTTTCTGTGAAGATCATTAATTACG 840
Qy 281 CysProAlaProIleLeuIysGluValGlyMetIysAlaAlaLeuGlnValSerMetAsn 300
Db 841 TGTCCAGCCCTATCTTAATAAAGATGSCATGAAAGCTGCATCCAGTCCAGTCAGCATGAAC 900
Qy 301 AspGlyLeuSerPheIleSerSerSerValIleIleIleThrThrIleCysSerAspGly 320
Db 901 GATGACCTCTCTTTATCTCCAGTTCTGTGCATCATCACCAACACACTGTTCTCCCAA 960
Qy 321 Ser 321
Db 961 TCT 963
RESULT 14
US-10-038-307-23
; Sequence 23, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-23
Alignment Scores:
Pred. No.: 1,23e-204 Length: 1056
Score: 1649.00 Matches: 318
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.15% Indels: 0
DB: 15 Gaps: 0
US-09-970-076-2 (1-368) x US-10-038-307-23 (1-1056)
Qy 1 MetAlaThrAlaGluArgAlaAlaLeuGlyIleGlyPheGlnTrpLeuSerIleuAlaThr 20
Db 13 ATGGCCACCGCGCGAGCGGAGACCCCTCGCATCGGCTTCACATGGCTCTCTTGGCCACT 72
Qy 21 LeuValIleuIleCysAlaGlyGlnGlyArgArgGluAsnGlyGlyProAlaCysTyr 40
Db 73 CTGGGCTCATCTGGCCCGGCAAGGGGAGACGAGGAGAGAGGGGCTCCAGCTGCTAC 132
Qy 41 GlyGlyPheAspLeuTyrPheIleLeuAspIysSerGlySerValLeuHisIleTrpAsn 60
Db 133 GCGGATTGACCTGATCTTCAATTTTGAACAAATCAGAAAGTGTGTGACCACTGGAAAT 192

Qy 61 GluIleTyrPheValGluGlnIleuAlaHisIysPheIleSerProGlnIleuArgMet 80
Db 193 GAATCTATTAATTCTGTGGAACAGTTGGCTGCAAAATTCATCAGCCCACTGGAATG 252
Qy 81 SerPheIleValPheSerThrArgGlyThrThrIleuMetIysLeuThrGluAspArgGlu 100
Db 253 TCTTTATTTGTTTCTTCCACCCGAGAAACAACCTTAAAGAACTGACAGAAACAGAGAA 312
Qy 101 GlnIleArgGlnGlyLeuGlnGlnIleuValIleuProGlyValAspThrIleuMet 120
Db 313 CAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATG 372
Qy 121 HisGlyIlePheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
Db 373 CATGAGATTTTGAAGAGCCCACTGACAGATTTATTTGAAAACAGCAAGAGATACAGG 432
Qy 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGlyAspLeuPhePheTyr 160
Db 433 ACAGCCAGCTCATCATGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 492
Qy 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db 493 TCAGAGAGGAGGCTTAATAGCTTCGAGATCTTGTCAAATTTTACTGTGTGTGTG 552
Qy 181 LysAspPheAsnGluThrGlnIleuAlaArgIleAlaAspSerIysAspHisValPhePro 200
Db 553 AAGATTTCATAGACACAGCTGCCCGGATTCGGGACAGTAAGATCATGTGTTCCC 612
Qy 201 ValaenaspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValysSerCys 220
Db 613 GTGAATGACGGCTTTCAGGCTCTGCAAGCATCATCCACTCAATTTTGAAGAAGTCTGC 672
Qy 221 IleguileleuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
Db 673 ATCGAATTTCTAGACGCTGAACCATCCACATATGTGAGAGAGATCTCAATTAATGTTC 732
Qy 241 ValaArgGlyAsnGlyPheArgHisAlaIleArgAsnValAspArgValLeuCysSerPheIys 260
Db 733 GTGAGAGAAACGGCTTCGACATCCGCAACGTGACAGGGTCTCTGCAAGCTTTCAG 792
Qy 261 IleAsnAspSerValThrIleuAsnGlyuysPropheSerValGluAspThrIleuLeu 280
Db 793 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGATCATTAATTACG 852
Qy 281 CysProAlaProIleLeuIysGluValGlyMetIysAlaAlaLeuGlnValSerMetAsn 300
Db 853 TGTCCAGCGCTCTATCTTAATAAAGATGTCATGAAAGCTGCATCCAGTCCAGTCAAGAAC 912
Qy 301 AspGlyLeuSerPheIleSerSerSerValIleIleIleThrThrIleCysSer 318
Db 913 GATGCTCTCTTTATCTCCAGTTCTGTGCATCATCACCAACCACTGTAAGC 966
RESULT 15
US-10-201-292-23
; Sequence 23, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-23

Alignment Scores:

Pred. No.:	1,236-204	Length:	1056
Score:	1649.00	Matches:	318
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	86.15%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-2 (1-368) x US-10-201-292-23 (1-1056)

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QY      1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db      13 ATGGCCAGGCGGAGAGACCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT   72
QY      21 LeuValLeuIleCyAlaGlyGlnGlyValArgGluAspGlyGlyProAlaCysTyr 40
Db      73 CTGGTGCCTCATCTGGCCGGGGAAGGGGACCGCAGAGAGATGGGGGTCCAGCCTGCCTAC 132
QY      41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db      133 GCGGATTTGACCTGTACTTCATTTTGGACAAATCAGAGAGTGTCTGCACACCTGGAAT 192
QY      61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
Db      193 GAAATCTATTACTTGTGTGAAACAGTTGGCTCCAAATTCATCAGCCACAGTTGAGAAATG 252
QY      81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db      253 TCCTTTATTTGTTTTCACCCGAGGAAACACCTTATGAAACTGACAGAAAGACAGAGAA 312
QY      101 GlnIleArgGlnGlyLeuGlnGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db      313 CAAATCCGTCAGAGCCCTAGAGAACTCCAGAAAGTTCTGCAGAGAGACACTTACATG 372
QY      121 HisGluGlyPheGluArgAlaSerGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
Db      373 CATGAAGGATTTGAAAGGCGCCAGTAGAGCATTTATGAAACAGCAAGGGTACAGG 432
QY      141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAspLeuPhePheTyr 160
Db      433 ACAGCCAGCGTCATCATTTGCTTTGACTGATGAGAACTCCATGAAAGATCTTTTTCAT 492
QY      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db      493 TCAGAGAGGAGGACTAATAGGCTCGAGATCTTGGTCATTTACTGTGTGTGTG 552
QY      181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db      553 AAAGATTTCAATGAGACACAGCTGGCCCGGATTCGGAACAGTAAAGATCATGTGTTTCC 612
QY      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
Db      613 GTGAATGACGGCTTTCAGGCTCTGCAGGCAATCCACTCAATTTTGAAGAAAGTCCCTGC 672
QY      221 IleGlnIleLeuAlaIleGluProSerThrIleCyAlaGlyGluSerPheGlnValVal 240
Db      673 ATCGAAATTTTAGCAGCTGAGACCATCCACATATGTGCAGAGAGACTCATTTCAAGTGTG 732
QY      241 ValArgGlyAsnGlyPheArgHisAlaIleArgAsnValAspArgValLeuCysSerPheLys 260
Db      733 GTGAGAGGAAACGGCTTCGACATGCCCGCAACGTGGACAGGGTCTCTGCAGCTTCAAG 792
QY      261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluAspThrTyrLeuLeu 280
Db      793 ATCAATGACTCGGTACACTCATAGAGAGCCCTTTCTGTGGAAGATCTTATTACTCG 852
QY      281 CysProAlaProIleLeuLysGlnValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db      853 TGTCCAGGCGCCATCTTAAAGAAAGTTGGCATGAAGCTGCACCTCAGGTCAAGCATGAAC 912
QY      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSer 318
Db      913 GATGGCTCTCTTTTATCTCCAGTTCTGTGCATCATCACACACACACTGTAGC 966
```

Search completed: June 22, 2004, 08:10:30
Job time : 571.154 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:39:51 ; Search time 13.8962 Seconds

(without alignment)

Title: US-09-970-076-2

Perfect score: 1914
Sequence: 1 MATBRRLAGTGFQWLSLAT.....VIVKEVPPPAESENKIK 368

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCUTS_COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	8.7	1155	1	US-08-286-889-46
2	166	8.7	1155	1	US-08-485-618-46
3	166	8.7	1155	1	US-08-362-652-46
4	166	8.7	1155	2	US-08-605-672-46
5	166	8.7	1155	2	US-08-482-293A-46
6	166	8.7	1155	2	US-08-943-363-46
7	166	8.7	1155	3	US-09-193-043-46
8	166	8.7	1155	4	US-09-688-307A-46
9	166	8.7	1155	4	US-09-350-259-46
10	166	8.7	1161	1	US-08-485-618-53
11	166	8.7	1161	1	US-08-362-652-53
12	166	8.7	1161	2	US-08-605-672-53
13	166	8.7	1161	2	US-08-482-293A-53
14	166	8.7	1161	3	US-08-943-363-53
15	166	8.7	1161	3	US-09-193-043-53
16	166	8.7	1161	4	US-09-688-307A-53
17	166	8.7	1161	4	US-09-350-259-53
18	159.5	8.3	1151	1	US-08-286-889-37
19	159.5	8.3	1151	1	US-08-485-618-37
20	159.5	8.3	1151	1	US-08-362-652-37
21	159.5	8.3	1151	2	US-08-605-672-37
22	159.5	8.3	1151	2	US-08-482-293A-37
23	159.5	8.3	1151	2	US-08-943-363-37
24	159.5	8.3	1151	3	US-09-193-043-37
25	159.5	8.3	1151	4	US-09-688-307A-37
26	159.5	8.3	1151	4	US-09-350-259-37
27	159.5	8.3	1161	1	US-08-173-497-2

28	159.5	8.3	1161	1	US-08-286-889-2	Sequence 2, Appl1
29	159.5	8.3	1161	1	US-08-485-618-2	Sequence 2, Appl1
30	159.5	8.3	1161	1	US-08-485-618-55	Sequence 55, Appl1
31	159.5	8.3	1161	1	US-08-485-618-99	Sequence 99, Appl1
32	159.5	8.3	1161	1	US-08-362-652-2	Sequence 2, Appl1
33	159.5	8.3	1161	1	US-08-362-652-55	Sequence 55, Appl1
34	159.5	8.3	1161	2	US-08-605-672-2	Sequence 2, Appl1
35	159.5	8.3	1161	2	US-08-605-672-55	Sequence 55, Appl1
36	159.5	8.3	1161	2	US-08-482-293A-2	Sequence 2, Appl1
37	159.5	8.3	1161	2	US-08-482-293A-55	Sequence 55, Appl1
38	159.5	8.3	1161	2	US-08-482-293A-99	Sequence 99, Appl1
39	159.5	8.3	1161	2	US-08-943-363-2	Sequence 2, Appl1
40	159.5	8.3	1161	2	US-08-943-363-55	Sequence 55, Appl1
41	159.5	8.3	1161	2	US-08-943-363-99	Sequence 99, Appl1
42	159.5	8.3	1161	3	US-09-193-043-2	Sequence 2, Appl1
43	159.5	8.3	1161	3	US-09-193-043-55	Sequence 55, Appl1
44	159.5	8.3	1161	3	US-09-193-043-99	Sequence 99, Appl1
45	159.5	8.3	1161	3	US-09-193-043-99	Sequence 99, Appl1

ALIGNMENTS

RESULT 1

US-08-286-889-46

Sequence 46, Application US/08286889

Patent No. 5470953

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Mich

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Seair Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286, 889

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: P38,659

REFERENCE/DOCKET NUMBER: 27866/32168

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 1155 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-286-889-46

Query Match 8.7% Score 166; DB 1; Length 1155;

Best Local Similarity 28.2%; Pred. No. 7.6e-09;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

37 PACYV-GPDLYFLDKSGSV-LHMHNEIYVFEQIAHKFISPOLRMSFVSTRTTLMK 94

Db 144 PEGCGEMDIAFLIDSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMOYSNLIKTHFT 203
Qy 95 LTEDR-----EQIROGJLELOKVLPGGDTYMHGFERASBOIYYENRGYRTA-SVIAL 148
Db 204 PTEFKSSLSPOSIVDAIVQLO-----GLTYTASGIQKVVELFHSKNGARKSACKILIVI 258
Qy 149 TDGELHEDLFFYSB--REANRSRDLGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 199
Db 259 TDGQKFRDPLEYRHHVPEAKA---GIIRYAIQGDAPREPTALQELNTIGSAPSQDHVF 315
Qy 200 PVDNGFOLGIIHSILKSCIEILAAPSTICAGESFQVVRNGFRHARNVD 253
Db 316 KVGK-FVALRSIQROIQR-----IFALGTSSRSSSFQHEMSQEGSSALSMD 364

RESULT 2

US-08-485-618-46
; Sequence 46, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Seear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-618-46

Query Match 8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFIIDKSGSV-LHHMNEIYFVEQLAHFISPOLRMSFIYSTGTGLMK 94
Db 144 PEGCGEMDIAFLIDSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMOYSNLIKTHFT 203

Qy 95 LTEDR-----EQIROGJLELOKVLPGGDTYMHGFERASBOIYYENRGYRTA-SVIAL 148
Db 204 PTEFKSSLSPOSIVDAIVQLO-----GLTYTASGIQKVVELFHSKNGARKSACKILIVI 258
Qy 149 TDGELHEDLFFYSB--REANRSRDLGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 199
Db 259 TDGQKFRDPLEYRHHVPEAKA---GIIRYAIQGDAPREPTALQELNTIGSAPSQDHVF 315
Qy 200 PVDNGFOLGIIHSILKSCIEILAAPSTICAGESFQVVRNGFRHARNVD 253
Db 316 KVGK-FVALRSIQROIQR-----IFALGTSSRSSSFQHEMSQEGSSALSMD 364

RESULT 3

US-08-362-652-46
; Sequence 46, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Seear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,652
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-362-652-46

Query Match 8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFIIDKSGSV-LHHMNEIYFVEQLAHFISPOLRMSFIYSTGTGLMK 94
Db 144 PEGCGEMDIAFLIDSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMOYSNLIKTHFT 203
Qy 95 LTEDR-----EQIROGJLELOKVLPGGDTYMHGFERASBOIYYENRGYRTA-SVIAL 148
Db 204 PTEFKSSLSPOSIVDAIVQLO-----GLTYTASGIQKVVELFHSKNGARKSACKILIVI 258
Qy 149 TDGELHEDLFFYSB--REANRSRDLGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 199

Db 259 TDGQFRDPLEYRHYIPEAEKA---GIRYVAIGVDAPREPTALQELMTIGSAPQDHVF 315
QY 200 PVDGFOALQGIHSHILKKSCEIILAEPTICAGESFQVVRNGGFHARND 253
Db 316 KVG-N-FVALRSTIQIOEK-----IFAIGTESRSSSSFOHMSQGFSSALSMO 364

RESULT 4

US-08-605-672-46
Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-46

Query Match 8.7%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYV-GPDLYFILDKSGSV-LHHNNEIYFVEQLAHKFIISPOLMSFVSTRTGTTLMK 94
Db 144 PECPOEMDIAPLIDGSSIDSDPTOMDFVKALMGQLASTSTSFSLMOYSNIIKTHFT 203
QY 95 LTEDR-----EIQRLGLELQKVLPGDPTVMHEGFERASEQIYYENRGYRTA-SVIAL 148
Db 204 FTEFKSSLSPOSLVDALVOLQ-----GLTYTASGIQVKELFHSKNGARKSAKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDLGAIYVCVYKD-FNE-TOLARI-----ADSKDHVF 199
Db 259 TDGQFRDPLEYRHYIPEAEKA---GIRYVAIGVDAPREPTALQELMTIGSAPQDHVF 315

QY 200 PVDGFOALQGIHSHILKKSCEIILAEPTICAGESFQVVRNGGFHARND 253
Db 316 KVG-N-FVALRSTIQIOEK-----IFAIGTESRSSSSFOHMSQGFSSALSMO 364

RESULT 5

US-08-482-293A-46
Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-46

Query Match 8.7%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYV-GPDLYFILDKSGSV-LHHNNEIYFVEQLAHKFIISPOLMSFVSTRTGTTLMK 94
Db 144 PECPOEMDIAPLIDGSSIDSDPTOMDFVKALMGQLASTSTSFSLMOYSNIIKTHFT 203
QY 95 LTEDR-----EIQRLGLELQKVLPGDPTVMHEGFERASEQIYYENRGYRTA-SVIAL 148
Db 204 FTEFKSSLSPOSLVDALVOLQ-----GLTYTASGIQVKELFHSKNGARKSAKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDLGAIYVCVYKD-FNE-TOLARI-----ADSKDHVF 199
Db 259 TDGQFRDPLEYRHYIPEAEKA---GIRYVAIGVDAPREPTALQELMTIGSAPQDHVF 315
QY 200 PVDGFOALQGIHSHILKKSCEIILAEPTICAGESFQVVRNGGFHARND 253

Db 316 KVGK-FVALRSIQIOEK-----IPALGTESSSSSFQHEMSQGFSSALSMD 364

RESULT 6
US-08-943-363-46
Sequence 46, Application US/08943363

Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5837478 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-46

Query Match 8.7%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLDKSGSV-LHHMNEIYFVEQLAHKFTSPQRMSPYVSTGTTLMK 94
Db 144 PECQGEQMDIAFLIDSGSIDQSDPTQKDFVKALMGQLASTSTSFSLMOYSNLTKHT 203
Qy 95 LTEDR-----EOLRGLEELQKVLPGDPTVMHEGFERASEOIYENRGYRTA-SVIAL 148
Db 204 FTEFKSSLSPOSLVDALVQLQ-----GLTYTASGIQKVKELFHSKNGARSAKILIVI 258
Qy 149 TDGELHEDLFPYSE--REANRSRDGAIVYCVGYKD-FNE-TOLARI-----ADSKDHVF 199
Db 259 TDGQKFRDPLEYRHYIPEAEKA---GIIRYALGVGDAPREPTALQELNTIGSAPSQDHVF 315
Qy 200 PVNDGFOALOGIHSILKSCIEILAEPTICAGESFOVVRNGGFRHARNVD 253
Db 316 KVGK-FVALRSIQIOEK-----IPALGTESSSSSFQHEMSQGFSSALSMD 364

RESULT 7
US-09-193-043-46
Sequence 46, Application US/09193043

Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6251395 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-193-043-46

Query Match 8.7%; Score 166; DB 3; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLDKSGSV-LHHMNEIYFVEQLAHKFTSPQRMSPYVSTGTTLMK 94
Db 144 PECQGEQMDIAFLIDSGSIDQSDPTQKDFVKALMGQLASTSTSFSLMOYSNLTKHT 203
Qy 95 LTEDR-----EOLRGLEELQKVLPGDPTVMHEGFERASEOIYENRGYRTA-SVIAL 148
Db 204 FTEFKSSLSPOSLVDALVQLQ-----GLTYTASGIQKVKELFHSKNGARSAKILIVI 258
Qy 149 TDGELHEDLFPYSE--REANRSRDGAIVYCVGYKD-FNE-TOLARI-----ADSKDHVF 199
Db 259 TDGQKFRDPLEYRHYIPEAEKA---GIIRYALGVGDAPREPTALQELNTIGSAPSQDHVF 315
Qy 200 PVNDGFOALOGIHSILKSCIEILAEPTICAGESFOVVRNGGFRHARNVD 253
Db 316 KVGK-FVALRSIQIOEK-----IPALGTESSSSSFQHEMSQGFSSALSMD 364

RESULT 8
US-09-688-307A-46
Sequence 46, Application US/09688307A

Patent No. 6432404
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6432404 Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR FILING DATE: 1997-10-03

NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-688-307A-46

Query Match 8.7%; Score 166; DB 4; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GRDLYFLDKSGSV-LHMNEIYFVEQALAHKFIISPOLMSTFVSTRTGTTLMK 94
DB 144 PECQEGENDIAFLIDGSSSIDOSDPTQMKDFKALMGQLASTSTSFSLMOYSNLIKTHFT 203
QY 95 LTEDR-----EQIRGLELQKVLPGDPTVMHEGFERASEQIYYENRGYRTA-SVIAL 148
DB 204 FTEFSSLSPOSIVDAIVQLQ-----GLTYASGIQKVKELFHSKNGARKSAKKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGVND-FNE-TOLARI-----ADSKDHVF 199
DB 259 TDGQFRPDLRYRHVIPAERKA--GIIRYALGVGDAREPTALQELMTTIGSAPSDHVF 315
QY 200 PVNDGFOALOGIHSILKSCIEILAEPTICAGESFOVVVRNGGFRHARVD 253
DB 316 KVGK-FVALRSTQRIQIEK---IFALIGTSSRSSSFQHEMSSQEGFSALSM 364

RESULT 9

US-09-350-259-46
Sequence 46; Application US/09350259
Patent No. 6620915
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6620915el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-350-259-46

Query Match 8.7%; Score 166; DB 4; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GRDLYFLDKSGSV-LHMNEIYFVEQALAHKFIISPOLMSTFVSTRTGTTLMK 94
DB 144 PECQEGENDIAFLIDGSSSIDOSDPTQMKDFKALMGQLASTSTSFSLMOYSNLIKTHFT 203
QY 95 LTEDR-----EQIRGLELQKVLPGDPTVMHEGFERASEQIYYENRGYRTA-SVIAL 148
DB 204 FTEFSSLSPOSIVDAIVQLQ-----GLTYASGIQKVKELFHSKNGARKSAKKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGVND-FNE-TOLARI-----ADSKDHVF 199
DB 259 TDGQFRPDLRYRHVIPAERKA--GIIRYALGVGDAREPTALQELMTTIGSAPSDHVF 315

QY 200 PVNDGFOALOGIHSILKSCIEILAEPTICAGESFOVVVRNGGFRHARVD 253
DB 316 KVGK-FVALRSTQRIQIEK---IFALIGTSSRSSSFQHEMSSQEGFSALSM 364

RESULT 10

US-08-485-618-53
Sequence 53; Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-0448
TELEFAX: 312-474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-53

Query Match 8.7%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GRDLYFLDKSGSV-LHMNEIYFVEQALAHKFIISPOLMSTFVSTRTGTTLMK 94
DB 144 PECQEGENDIAFLIDGSSSIDOSDPTQMKDFKALMGQLASTSTSFSLMOYSNLIKTHFT 203
QY 95 LTEDR-----EQIRGLELQKVLPGDPTVMHEGFERASEQIYYENRGYRTA-SVIAL 148
DB 204 FTEFSSLSPOSIVDAIVQLQ-----GLTYASGIQKVKELFHSKNGARKSAKKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGVND-FNE-TOLARI-----ADSKDHVF 199
DB 259 TDGQFRPDLRYRHVIPAERKA--GIIRYALGVGDAREPTALQELMTTIGSAPSDHVF 315
QY 200 PVNDGFOALOGIHSILKSCIEILAEPTICAGESFOVVVRNGGFRHARVD 253

Db 316 KVG-N-FVALRSIQROIQEK-----IFAIGCTSSRSSSSSFQHMSEOGCFSSALSMD 364

RESULT 11

US-08-362-652-53
Sequence 53, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-53

Query Match 8.7%; Score 166; DB 1; Length 1161;

Best Local Similarity 28.2%; Pred. No. 7.6e-09; Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGLMK 94
Db 144 PECGQGMEDIAFLIDGSSSIDQSDFTQMKDFVALMQLASTSTSFILMQYSNLKTHFT 203
Qy 95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHGFEFASQIYYENQGYRTA-SVIAL 148
Db 204 FTEFKSSLSPOSIVDAIVQIQ-----GLTYTASGIQKVVLELPHSKNGARKSAKKIILIVI 258
Qy 149 TDGELHEDLFFYSE--REANRSRDLGAIYVCVVKD-FNE-TOLARI-----ADSKDHF 199
Db 259 TDGQKFRDPLEYRHVIPAERA---GIIRYALIGVDAREPTALQELNTIGSAPSQDHVF 315
Qy 200 PVNDGFOALGIIHSILKSCIEILAAEPSTICAGESFOVVVVGNGFRHARNVD 253
Db 316 KVG-N-FVALRSIQROIQEK-----IFAIGCTSSRSSSSSFQHMSEOGCFSSALSMD 364

RESULT 12

US-08-605-672-53
Sequence 53, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-53

Query Match 8.7%; Score 166; DB 2; Length 1161;

Best Local Similarity 28.2%; Pred. No. 7.6e-09; Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGLMK 94
Db 144 PECGQGMEDIAFLIDGSSSIDQSDFTQMKDFVALMQLASTSTSFILMQYSNLKTHFT 203
Qy 95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHGFEFASQIYYENQGYRTA-SVIAL 148
Db 204 FTEFKSSLSPOSIVDAIVQIQ-----GLTYTASGIQKVVLELPHSKNGARKSAKKIILIVI 258
Qy 149 TDGELHEDLFFYSE--REANRSRDLGAIYVCVVKD-FNE-TOLARI-----ADSKDHF 199
Db 259 TDGQKFRDPLEYRHVIPAERA---GIIRYALIGVDAREPTALQELNTIGSAPSQDHVF 315
Qy 200 PVNDGFOALGIIHSILKSCIEILAAEPSTICAGESFOVVVVGNGFRHARNVD 253
Db 316 KVG-N-FVALRSIQROIQEK-----IFAIGCTSSRSSSSSFQHMSEOGCFSSALSMD 364

RESULT 13

US-08-482-293A-53
Sequence 53, Application US/08482293A


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; Patent No. 5831029
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,293A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-482-293A-53

Query Match      8.7%; Score 166; DB 2; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GFDLYFLIDKSSV-LHHNNEIYFVEQLAHKFISPOLRMSFTVSTGTITMK 94
DB 144 PECQOEMDIADFLIDGSSIDQSDFTQMKDFKALMGQLASTSTFSIMQYSNLIKHTFT 203
QY 95 LTEDR-----EQIRGLEELQKVLPGDPTVMHEGPERASEQIYYENRGYRTA-SVITL 148
DB 204 FTERKSSISPOSIVDAIVQLQ-----GLTYASGIQKVKELFKNGARKSAAKILIVI 258
QY 149 TDGEIHEDLFFYSR--REANRSRDGAIVYCVGVD-FNE-TOLARI-----ADSKDHF 199
DB 259 TDGQKFRPPLRYRHYVPEAKA---GIRYAGVGDAREPPLALQELNTIGSAPSDHVF 315
QY 200 PVNDGFOLQGIHISILKSCIEILAEPSITCAGESFOVVVRNGRFRHARNVD 253
DB 316 KVGN-FVALRSIORIOEK---IFAIGTESRSSSFQHEMSQEGFSSALSMD 364

```

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; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-943-363-53

Query Match      8.7%; Score 166; DB 2; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7.6e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GFDLYFLIDKSSV-LHHNNEIYFVEQLAHKFISPOLRMSFTVSTGTITMK 94
DB 144 PECQOEMDIADFLIDGSSIDQSDFTQMKDFKALMGQLASTSTFSIMQYSNLIKHTFT 203
QY 95 LTEDR-----EQIRGLEELQKVLPGDPTVMHEGPERASEQIYYENRGYRTA-SVITL 148
DB 204 FTERKSSISPOSIVDAIVQLQ-----GLTYASGIQKVKELFKNGARKSAAKILIVI 258
QY 149 TDGEIHEDLFFYSR--REANRSRDGAIVYCVGVD-FNE-TOLARI-----ADSKDHF 199
DB 259 TDGQKFRPPLRYRHYVPEAKA---GIRYAGVGDAREPPLALQELNTIGSAPSDHVF 315
QY 200 PVNDGFOLQGIHISILKSCIEILAEPSITCAGESFOVVVRNGRFRHARNVD 253
DB 316 KVGN-FVALRSIORIOEK---IFAIGTESRSSSFQHEMSQEGFSSALSMD 364

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RESULT 14
US-08-943-363-53
; Sequence 53, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica

```

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RESULT 15
US-09-193-043-53
; Sequence 53, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica

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;; TITLE OF INVENTION: No. 6251395a1 Human 2
;; FILE REFERENCE: 27866/35004
;; CURRENT APPLICATION NUMBER: US/09/193,043
;; CURRENT FILING DATE: 1998-11-16
;; EARLIER APPLICATION NUMBER: 08/173,497
;; EARLIER FILING DATE: 1993-12-23
;; EARLIER APPLICATION NUMBER: 08/286,889
;; EARLIER FILING DATE: 1994-08-05
;; EARLIER APPLICATION NUMBER: 08/362,652
;; EARLIER FILING DATE: 1994-12-21
;; EARLIER APPLICATION NUMBER: 08/343,363
;; EARLIER FILING DATE: 1997-10-03
;; NUMBER OF SEQ ID NOS: 114
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 53
;; LENGTH: 1161
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-193-043-53

Query Match 8.7%; Score 166; DB 3; Length 1161;

Best Local Similarity 28.2%; Pred. No. 7.6e-09; Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

OY 37 PACYG-GFDLYFLDKSGSV-LHWNELIYFVEQLAHKFISPQLMSFIVFSTRTTLMK 94
DB 144 PECPQEMDI AFLIDGSGSIDQSDFTQKMDFKALMQLASTSFSIMQYSNIIKTHFT 203
OY 95 LTEDR-----EQIRGLEELQKVLPGDPTMHGEFPERASEQIYYENRGYRTA-SVITAL 148
DB 204 FTEFKSSLSPOSVDATVQLQ----GLTYASGIQKVVELFHSKNGARKSAKKILIVI 258
OY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGVKD-FNE-TOLARI-----ADSKDHVF 199
DB 259 TDGQKFRDPLEYRHYIPAEKA---GIIRVAIGVDAREPTALQELNTIGSAPSQDHVF 315
OY 200 PVNDGFQALQGIHSLKSCIEIILAEFSTICAGESFQVVVRNGEFRHARNVD 253
DB 316 KVGN-FVALRSIQRIQEK---IPAIETGTSRSSSSSFQHEMSQEGFSSALSM 364

Search completed: June 21, 2004, 13:46:34

Job time : 14.8962 secs

Qy 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Db 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Qy 301 DGLSFISSSVITTTTCS 318
Db 301 DGLSFISSSVITTTTCS 318

RESULT 14
US-10-038-307-24

; Sequence 24, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Englin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-038-307-24

Query Match 86.2%; Score 1649; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 2,5e-162;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPA CYGFPDLYFLDKSGSVLHNMN 60
Db 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPA CYGFPDLYFLDKSGSVLHNMN 60
Qy 61 EIIYFVEQLAKHFTSPQRMSPFIVSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
Db 61 EIIYFVEQLAKHFTSPQRMSPFIVSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
Qy 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIYCVGV 180
Db 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIYCVGV 180
Qy 181 KDFNETQARLADSKDHFVPVNDGFQALQGIHSLKSCIEIIAEPSTICAGESFQV 240
Db 181 KDFNETQARLADSKDHFVPVNDGFQALQGIHSLKSCIEIIAEPSTICAGESFQV 240
Qy 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Db 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Qy 301 DGLSFISSSVITTTTCS 318
Db 301 DGLSFISSSVITTTTCS 318

RESULT 15
US-10-201-292-24

; Sequence 24, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Englin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-201-292-24

Query Match 86.2%; Score 1649; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 2,5e-162;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPA CYGFPDLYFLDKSGSVLHNMN 60
Db 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPA CYGFPDLYFLDKSGSVLHNMN 60
Qy 61 EIIYFVEQLAKHFTSPQRMSPFIVSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
Db 61 EIIYFVEQLAKHFTSPQRMSPFIVSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
Qy 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIYCVGV 180
Db 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIYCVGV 180
Qy 181 KDFNETQARLADSKDHFVPVNDGFQALQGIHSLKSCIEIIAEPSTICAGESFQV 240
Db 181 KDFNETQARLADSKDHFVPVNDGFQALQGIHSLKSCIEIIAEPSTICAGESFQV 240
Qy 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Db 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Qy 301 DGLSFISSSVITTTTCS 318
Db 301 DGLSFISSSVITTTTCS 318

Search completed: June 21, 2004, 14:02:12
Job time : 38.7256 secs

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; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12
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Query Match      86.2%; Score 1649; DB 10; Length 333;
Best Local Similarity 100.0%; Pred. No. 2,4e-162;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACGFDLYTLDKSGSVLHHMN 60
Db 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACGFDLYTLDKSGSVLHHMN 60
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Db 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRGTTMLKLTEDREQIRQGLELQVLPBGDTYM 120
Oy 121 HEGPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIVYCVGV 180
Db 121 HEGPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIVYCVGV 180
Oy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
Oy 241 VRGNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Db 241 VRGNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Oy 301 DGLSFISISSVITTTTHCS 318
Db 301 DGLSFISISSVITTTTHCS 318
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RESULT 12
US-10-038-307-2
; Sequence 2, Application US/10038307
; Publication No. US20030134786a1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-038-307-2
```

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Query Match      86.2%; Score 1649; DB 14; Length 333;
Best Local Similarity 100.0%; Pred. No. 2,4e-162;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACGFDLYTLDKSGSVLHHMN 60
Db 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACGFDLYTLDKSGSVLHHMN 60
Oy 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRGTTMLKLTEDREQIRQGLELQVLPBGDTYM 120
Db 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRGTTMLKLTEDREQIRQGLELQVLPBGDTYM 120
Oy 121 HEGPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIVYCVGV 180
Db 121 HEGPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIVYCVGV 180
Oy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
Oy 241 VRGNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Db 241 VRGNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Oy 301 DGLSFISISSVITTTTHCS 318
Db 301 DGLSFISISSVITTTTHCS 318
```

```

RESULT 13
US-10-201-292-2
; Sequence 2, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-2
```

```

Query Match      86.2%; Score 1649; DB 14; Length 333;
Best Local Similarity 100.0%; Pred. No. 2,4e-162;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Oy 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACGFDLYTLDKSGSVLHHMN 60
Db 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACGFDLYTLDKSGSVLHHMN 60
Oy 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRGTTMLKLTEDREQIRQGLELQVLPBGDTYM 120
Db 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRGTTMLKLTEDREQIRQGLELQVLPBGDTYM 120
Oy 121 HEGPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIVYCVGV 180
Db 121 HEGPERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIVYCVGV 180
Oy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
```

Db 307 SVIITTHCSGSIILALVLFLLALALALMWFWPLCCTVIIEKVPPEESEE 362

RESULT 9

US-10-038-307-18

Sequence 18, Application US/10038307

Publication No. US20030134786A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 551

TYPE: PRT

ORGANISM: Homo sapiens

US-10-038-307-18

Query Match 86.8%; Score 1661; DB 14; Length 551;

Best Local Similarity 100.0%; Pred. No. 3e-163;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATARRALGIGFQWLSLATTVLVLCAGGCGRRREDGCPACYGFDLYFLIDKSGSVLHHMN 60

Db 1 MATARRALGIGFQWLSLATTVLVLCAGGCGRRREDGCPACYGFDLYFLIDKSGSVLHHMN 60

Qy 61 EIIYFVEQLAHKFI SPOLRMSFI VSTRTGTTLMKLTEDREQIRGLBELOKVLPGDPTM 120

Db 61 EIIYFVEQLAHKFI SPOLRMSFI VSTRTGTTLMKLTEDREQIRGLBELOKVLPGDPTM 120

Qy 61 EIIYFVEQLAHKFI SPOLRMSFI VSTRTGTTLMKLTEDREQIRGLBELOKVLPGDPTM 120

Db 61 EIIYFVEQLAHKFI SPOLRMSFI VSTRTGTTLMKLTEDREQIRGLBELOKVLPGDPTM 120

Qy 121 HEGFERASEQIYYENROGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVGV 180

Db 121 HEGFERASEQIYYENROGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVGV 180

Qy 121 HEGFERASEQIYYENROGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVGV 180

Db 121 HEGFERASEQIYYENROGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVGV 180

Qy 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABSTICAGESFGV 240

Db 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABSTICAGESFGV 240

Qy 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Db 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Qy 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Db 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Qy 301 DGLSFISSSVITTTTHCSDG 320

Db 301 DGLSFISSSVITTTTHCSDG 320

RESULT 10

US-10-201-292-18

Sequence 18, Application US/10201292

Publication No. US20030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 551

TYPE: PRT

ORGANISM: Homo sapiens

US-10-201-292-18

Query Match 86.8%; Score 1661; DB 14; Length 551;

Best Local Similarity 100.0%; Pred. No. 3e-163;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATARRALGIGFQWLSLATTVLVLCAGGCGRRREDGCPACYGFDLYFLIDKSGSVLHHMN 60

Db 1 MATARRALGIGFQWLSLATTVLVLCAGGCGRRREDGCPACYGFDLYFLIDKSGSVLHHMN 60

Qy 61 EIIYFVEQLAHKFI SPOLRMSFI VSTRTGTTLMKLTEDREQIRGLBELOKVLPGDPTM 120

Db 61 EIIYFVEQLAHKFI SPOLRMSFI VSTRTGTTLMKLTEDREQIRGLBELOKVLPGDPTM 120

Qy 61 EIIYFVEQLAHKFI SPOLRMSFI VSTRTGTTLMKLTEDREQIRGLBELOKVLPGDPTM 120

Db 61 EIIYFVEQLAHKFI SPOLRMSFI VSTRTGTTLMKLTEDREQIRGLBELOKVLPGDPTM 120

Qy 121 HEGFERASEQIYYENROGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVGV 180

Db 121 HEGFERASEQIYYENROGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVGV 180

Qy 121 HEGFERASEQIYYENROGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVGV 180

Db 121 HEGFERASEQIYYENROGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVGV 180

Qy 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABSTICAGESFGV 240

Db 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABSTICAGESFGV 240

Qy 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Db 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Qy 301 DGLSFISSSVITTTTHCSDG 320

Db 301 DGLSFISSSVITTTTHCSDG 320

RESULT 11

US-09-796-753-12

Sequence 12, Application US/09796753

Publication No. US20030027998A1

GENERAL INFORMATION:

APPLICANT: McCarthy, Sean A.

TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

FILE REFERENCE: 7853-227-999

CURRENT APPLICATION NUMBER: US/09/796,753

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 09/183,175

PRIOR FILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: 09/223,094

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/223,546

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/224,246

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/259,388

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/122,458

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: 09/312,359

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 09/336,536

PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 09/342,687

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 09/345,464

PRIOR FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: 09/365,164

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/399,723

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 09/409,634

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 09/471,179

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 09/474,071

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/474,072

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/514,010

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (368)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-833-245-620

Query Match 97.7%; Score 1870; DB 11; Length 403;
 Best Local Similarity 96.1%; Pred. No. 5.8e-177;
 Matches 360; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAERRALGIGFOWLSLATTVLICAGGGRREDGPAACGFDLYFLIDKSGSVLHHNN 60
 DB 1 MATERRALGIGFOWLSLATTVLICAGGGRREDGPAACGFDLYFLIDKSGSVLHHNN 60
 QY 61 EIIYFVEOLANKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDVTYM 120
 DB 61 EIIYFVEOLANKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDVTYM 120
 QY 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGV 180
 DB 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGV 180
 QY 181 KDFNETOLARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGSPQV 240
 DB 181 KDFNETOLARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGSPQV 240
 QY 241 VRNGFRHARVNDVLCSPKINDSVTLNEKPSVEDTYLCPAPILKEVGKAAALQVSMN 300
 DB 241 VRNGFRHARVNDVLCSPKINDSVTLNEKPSVEDTYLCPAPILKEVGKAAALQVSMN 300
 QY 301 DGLSFISGVITTHGSDGSLATLAILFLLALALMMFWPLCCTVVIKEVPPPAE 360
 DB 301 DGLSFISGVITTHGSDGSLATLAILFLLALALMMFWPLCCTVVIKEVPPPAE 360
 QY 361 ESE 363
 DB 361 ESE 363

RESULT 7
 US-09-918-715-194
 Sequence 194, Application US/09918715
 Publication No. US20030017157A1
 GENERAL INFORMATION:
 APPLICANT: Brad St. Croix
 APPLICANT: Bert Vogelstein
 APPLICANT: Kenneth Kinzler
 TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 FILE REFERENCE: 1107.00134
 CURRENT APPLICATION NUMBER: US/09/918,715
 CURRENT FILING DATE: 2001-08-01
 PRIOR APPLICATION NUMBER: 60/222,599
 PRIOR FILING DATE: 2000-08-02
 PRIOR APPLICATION NUMBER: 60/224,360
 PRIOR FILING DATE: 2000-08-11
 PRIOR APPLICATION NUMBER: 60/282,850
 PRIOR FILING DATE: 2000-04-11
 NUMBER OF SEQ ID NOS: 358
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 194
 LENGTH: 562
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-918-715-194

Query Match 93.7%; Score 1793; DB 12; Length 562;
 Best Local Similarity 96.1%; Pred. No. 5.8e-177;
 Matches 342; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 9 LGIGFOWLSLATTVLICAGGGRREDGPAACGFDLYFLIDKSGSVLHHNNIYFVEQ 68
 DB 7 LGAGIRGLCVAAALVAVCAHGGRREDGPAACGFDLYFLIDKSGSVLHHNNIYFVEQ 66

QY 69 LAHKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDVTYMHGFERAS 128
 DB 67 LAHKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDVTYMHGFERAS 126
 QY 129 EQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGVXDFNETOL 188
 DB 127 EQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGVXDFNETOL 186
 QY 189 ARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGSPQVVRGNGFRH 248
 DB 187 ARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGSPQVVRGNGFRH 246
 QY 249 ARVNDVLCSPKINDSVTLNEKPSVEDTYLCPAPILKEVGKAAALQVSMNGLSFIS 308
 DB 247 ARVNDVLCSPKINDSVTLNEKPSVEDTYLCPAPILKEVGKAAALQVSMNGLSFIS 306
 QY 309 SVITTHGSDGSLATLAILFLLALALMMFWPLCCTVVIKEVPPPAESEE 364
 DB 307 SVITTHGSDGSLATLAILFLLALALMMFWPLCCTVVIKEVPPPAESEE 362

RESULT 8
 US-09-918-715-301
 Sequence 301, Application US/09918715
 Publication No. US20030017157A1
 GENERAL INFORMATION:
 APPLICANT: Brad St. Croix
 APPLICANT: Bert Vogelstein
 APPLICANT: Kenneth Kinzler
 TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 FILE REFERENCE: 1107.00134
 CURRENT APPLICATION NUMBER: US/09/918,715
 CURRENT FILING DATE: 2001-08-01
 PRIOR APPLICATION NUMBER: 60/222,599
 PRIOR FILING DATE: 2000-08-02
 PRIOR APPLICATION NUMBER: 60/224,360
 PRIOR FILING DATE: 2000-08-11
 PRIOR APPLICATION NUMBER: 60/282,850
 PRIOR FILING DATE: 2000-04-11
 NUMBER OF SEQ ID NOS: 358
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 301
 LENGTH: 562
 TYPE: PRT
 ORGANISM: Mouse
 US-09-918-715-301

Query Match 93.7%; Score 1793; DB 12; Length 562;
 Best Local Similarity 96.1%; Pred. No. 5.8e-177;
 Matches 342; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 9 LGIGFOWLSLATTVLICAGGGRREDGPAACGFDLYFLIDKSGSVLHHNNIYFVEQ 68
 DB 7 LGAGIRGLCVAAALVAVCAHGGRREDGPAACGFDLYFLIDKSGSVLHHNNIYFVEQ 66
 QY 69 LAHKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDVTYMHGFERAS 128
 DB 67 LAHKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDVTYMHGFERAS 126
 QY 129 EQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGVXDFNETOL 188
 DB 127 EQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGVXDFNETOL 186
 QY 189 ARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGSPQVVRGNGFRH 248
 DB 187 ARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGSPQVVRGNGFRH 246
 QY 249 ARVNDVLCSPKINDSVTLNEKPSVEDTYLCPAPILKEVGKAAALQVSMNGLSFIS 308
 DB 247 ARVNDVLCSPKINDSVTLNEKPSVEDTYLCPAPILKEVGKAAALQVSMNGLSFIS 306
 QY 309 SVITTHGSDGSLATLAILFLLALALMMFWPLCCTVVIKEVPPPAESEE 364
 DB 307 SVITTHGSDGSLATLAILFLLALALMMFWPLCCTVVIKEVPPPAESEE 362

```
RESULT 4
US-10-408-765A-1823
; Sequence 1823, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Choeh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1823
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1823

Query Match      99.0%; Score 1894; DB 16; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.9e-187;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATARRALGIGFQWLSLTLVLIACGGGRRREDGGPACYGFDLYFLIDKSGSVLHHMN 60
DB 1 MATARRALGIGFQWLSLTLVLIACGGGRRREDGGPACYGFDLYFLIDKSGSVLHHMN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDREIQGLLEQLVLPGGDTYM 120
DB 61 EIIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDREIQGLLEQLVLPGGDTYM 120
QY 121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLPFYSEREANSRDIGAIYVCYGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLPFYSEREANSRDIGAIYVCYGV 180
QY 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABPSTICAGBSFQV 240
DB 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABPSTICAGBSFQV 240
QY 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPFVEDTYLLCPAFLKEVGKKAALQVSMN 300
DB 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPFVEDTYLLCPAFLKEVGKKAALQVSMN 300
QY 301 DGLSFISSSVITTTTHCSGDSILAILLFLALLALMLMFWPLCCTVIIKEVPPPPAE 360
DB 301 DGLSFISSSVITTTTHCSGDSILAILLFLALLALMLMFWPLCCTVIIKEVPPPPAE 360
QY 361 ESEE 364
DB 361 ESEE 364

RESULT 5
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
```

```
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621

Query Match      98.7%; Score 1889; DB 11; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.7e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATARRALGIGFQWLSLTLVLIACGGGRRREDGGPACYGFDLYFLIDKSGSVLHHMN 60
DB 1 MATARRALGIGFQWLSLTLVLIACGGGRRREDGGPACYGFDLYFLIDKSGSVLHHMN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDREIQGLLEQLVLPGGDTYM 120
DB 61 EIIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDREIQGLLEQLVLPGGDTYM 120
QY 121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLPFYSEREANSRDIGAIYVCYGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLPFYSEREANSRDIGAIYVCYGV 180
QY 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABPSTICAGBSFQV 240
DB 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABPSTICAGBSFQV 240
QY 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPFVEDTYLLCPAFLKEVGKKAALQVSMN 300
DB 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPFVEDTYLLCPAFLKEVGKKAALQVSMN 300
QY 301 DGLSFISSSVITTTTHCSGDSILAILLFLALLALMLMFWPLCCTVIIKEVPPPPAE 360
DB 301 DGLSFISSSVITTTTHCSGDSILAILLFLALLALMLMFWPLCCTVIIKEVPPPPAE 360
QY 361 ESE 363
DB 361 ESE 363

RESULT 6
US-09-833-245-620
; Sequence 620, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 620
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (331)
```


Qy 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180
|
Db 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180
Qy 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240
|
Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240
Qy 241 VRGNGFRARAVNDVLCSPKINDSVTLNEKPSVEDTLLCPAPILKEVGKALQVSMN 300
|
Db 241 VRGNGFRARAVNDVLCSPKINDSVTLNEKPSVEDTLLCPAPILKEVGKALQVSMN 300
Qy 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVIIKEVPPPAE 360
|
Db 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVIIKEVPPPAE 360
Qy 361 ESEE 364
|
Db 361 ESEE 364

RESULT 2

US-09-918-715-232
; Sequence 232, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-232

Query Match 99.0%; Score 1894; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.9e-187;

Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPAACGPGDLYTILDKSGSVLHHMN 60
|
Db 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPAACGPGDLYTILDKSGSVLHHMN 60
Qy 61 EIVYFVEQLAHKFTSPQLRMSFIVSTRGTMLKLTEDREQIRQLELQVLPFGDPTM 120
|
Db 61 EIVYFVEQLAHKFTSPQLRMSFIVSTRGTMLKLTEDREQIRQLELQVLPFGDPTM 120
Qy 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180
|
Db 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180
Qy 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240
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Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240
Qy 241 VRGNGFRARAVNDVLCSPKINDSVTLNEKPSVEDTLLCPAPILKEVGKALQVSMN 300
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Qy 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVIIKEVPPPAE 360
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Db 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVIIKEVPPPAE 360

Db 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVIIKEVPPPAE 360
|
Qy 361 ESEE 364
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Db 361 ESEE 364

RESULT 3

US-10-301-822-199
; Sequence 199, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-029P2RM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-199

Query Match 99.0%; Score 1894; DB 14; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.9e-187;

Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPAACGPGDLYTILDKSGSVLHHMN 60
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Db 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPAACGPGDLYTILDKSGSVLHHMN 60
Qy 61 EIVYFVEQLAHKFTSPQLRMSFIVSTRGTMLKLTEDREQIRQLELQVLPFGDPTM 120
|
Db 61 EIVYFVEQLAHKFTSPQLRMSFIVSTRGTMLKLTEDREQIRQLELQVLPFGDPTM 120
Qy 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180
|
Db 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180
Qy 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240
|
Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240
Qy 241 VRGNGFRARAVNDVLCSPKINDSVTLNEKPSVEDTLLCPAPILKEVGKALQVSMN 300
|
Db 241 VRGNGFRARAVNDVLCSPKINDSVTLNEKPSVEDTLLCPAPILKEVGKALQVSMN 300
Qy 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVIIKEVPPPAE 360
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Db 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVIIKEVPPPAE 360
Qy 361 ESEE 364
|
Db 361 ESEE 364

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 13:44:26 ; Search time 36.7256 Seconds
(without alignments)
2828.859 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914
Sequence: 1 MATERRALGIGFQWLSLAT.....VILKEVPPPEASEENKIK 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1894	99.0	564	US-09-918-715-187	Sequence 187, App
2	1894	99.0	564	US-09-918-715-232	Sequence 232, App
3	1894	99.0	564	US-10-301-822-199	Sequence 199, App
4	1894	99.0	564	US-10-408-765A-1823	Sequence 1823, App
5	1889	98.7	403	US-09-833-245-621	Sequence 621, App
6	1870	97.7	403	US-09-833-245-620	Sequence 620, App
7	1793	93.7	562	US-09-918-715-194	Sequence 194, App
8	1793	93.7	562	US-09-918-715-301	Sequence 301, App
9	1661	86.8	551	US-10-038-307-18	Sequence 18, App1
10	1661	86.8	551	US-10-201-292-18	Sequence 18, App1
11	1649	86.2	333	US-09-796-753-12	Sequence 12, App1
12	1649	86.2	333	US-10-038-307-2	Sequence 2, App1
13	1649	86.2	333	US-10-201-292-2	Sequence 2, App1
14	1649	86.2	345	US-10-038-307-24	Sequence 24, App1
15	1649	86.2	345	US-10-201-292-24	Sequence 24, App1

16	1649	86.2	564	US-10-038-307-20	Sequence 20, App1
17	1649	86.2	564	US-10-201-292-20	Sequence 20, App1
18	1636	85.5	328	US-10-038-307-26	Sequence 26, App1
19	1636	85.5	328	US-10-201-292-26	Sequence 26, App1
20	1634.5	85.4	342	US-10-038-307-22	Sequence 22, App1
21	1634.5	85.4	342	US-10-201-292-22	Sequence 22, App1
22	1629	85.1	543	US-10-038-307-14	Sequence 14, App1
23	1629	85.1	543	US-10-038-307-16	Sequence 16, App1
24	1629	85.1	543	US-10-201-292-14	Sequence 14, App1
25	1629	85.1	543	US-10-201-292-16	Sequence 16, App1
26	1619	84.6	543	US-10-038-307-10	Sequence 10, App1
27	1619	84.6	543	US-10-201-292-10	Sequence 10, App1
28	1548	80.9	529	US-10-201-292-36	Sequence 36, App1
29	1488	77.7	534	US-10-038-307-12	Sequence 12, App1
30	1488	77.7	534	US-10-201-292-12	Sequence 12, App1
31	1434.5	74.9	504	US-10-201-292-32	Sequence 32, App1
32	1307	68.3	479	US-10-201-292-32	Sequence 32, App1
33	1193	62.3	460	US-10-201-292-28	Sequence 28, App1
34	1183	61.8	460	US-10-201-292-30	Sequence 30, App1
35	962.5	50.3	488	US-10-368-087-16	Sequence 16, App1
36	962.5	50.3	488	US-10-104-047-2639	Sequence 2639, App
37	957.5	50.0	488	US-09-796-753-52	Sequence 52, App1
38	957.5	50.0	488	US-10-038-307-6	Sequence 6, App1
39	957.5	50.0	488	US-10-201-292-6	Sequence 6, App1
40	938.5	49.0	587	US-09-764-870-312	Sequence 312, App
41	938.5	49.0	587	US-09-764-875-968	Sequence 968, App
42	938.5	49.0	587	US-10-125-540-312	Sequence 312, App
43	936.5	48.9	487	US-09-796-753-54	Sequence 54, App1
44	936.5	48.9	487	US-10-038-307-8	Sequence 8, App1
45	936.5	48.9	487	US-10-201-292-8	Sequence 8, App1

ALIGNMENTS

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RESULT 1
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Best Vogelstein
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-187
Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e-187;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPGACYGFDLYFTLDKSGSVLAHNN 60
Db 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPGACYGFDLYFTLDKSGSVLAHNN 60
QY 61 EIVYVEQLAKHFPISPOIRMSFIVSTGTMLKTLTEREQIRQGLEQLKVLPGSDRYM 120
Db 61 EIVYVEQLAKHFPISPOIRMSFIVSTGTMLKTLTEREQIRQGLEQLKVLPGSDRYM 120
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 22, 2004, 01:18:40 ; Search time 80.151 Seconds

(without alignments)
2547.963 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914

Sequence: 1 MATERRALGICFQWLSLAT.....VITKEVPPPAESENKIK 368

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued Patents NA -QFWT=Fastap -SUFFIX=trni -MINMATCH=0.1 -LOOPCL=0
-LDOEXT=0 -UNITS=File -START=1 -END=1 -MATRIX=blowm62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database: Issued Patents NA:

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5: /cgn2_6/ptodata/2/ina/6C.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1649	86.2	2459	4	US-09-833-381-998 Sequence 998, App
2	1592	72.7	1609	4	US-09-620-312D-8 Sequence 8, Appl
3	166	8.7	3519	1	US-08-286-889-45 Sequence 45, Appl
4	166	8.7	3519	1	US-08-485-618-45 Sequence 45, Appl
5	166	8.7	3519	1	US-08-362-652-45 Sequence 45, Appl
6	166	8.7	3519	1	US-08-605-672-45 Sequence 45, Appl
7	166	8.7	3519	2	US-08-482-293A-45 Sequence 45, Appl
8	166	8.7	3519	2	US-08-943-363-45 Sequence 45, Appl
9	166	8.7	3519	3	US-09-193-043-45 Sequence 45, Appl
10	166	8.7	3519	4	US-09-688-307A-45 Sequence 45, Appl
11	166	8.7	3519	4	US-09-350-259-45 Sequence 45, Appl
12	166	8.7	3803	1	US-08-485-618-52 Sequence 52, Appl

13	166	8.7	3803	1	US-08-362-652-52 Sequence 52, Appl
14	166	8.7	3803	1	US-08-605-672-52 Sequence 52, Appl
15	166	8.7	3803	2	US-08-482-293A-52 Sequence 52, Appl
16	166	8.7	3803	2	US-08-943-363-52 Sequence 52, Appl
17	166	8.7	3803	3	US-09-193-043-52 Sequence 52, Appl
18	166	8.7	3803	4	US-09-688-307A-52 Sequence 52, Appl
19	166	8.7	3803	4	US-09-350-259-52 Sequence 52, Appl
20	159.5	8.3	2499	1	US-08-485-618-96 Sequence 96, Appl
21	159.5	8.3	2499	1	US-08-605-672-96 Sequence 96, Appl
22	159.5	8.3	2499	2	US-08-482-293A-96 Sequence 96, Appl
23	159.5	8.3	2499	2	US-08-943-363-96 Sequence 96, Appl
24	159.5	8.3	2499	3	US-09-193-043-96 Sequence 96, Appl
25	159.5	8.3	2499	4	US-09-688-307A-96 Sequence 96, Appl
26	159.5	8.3	2499	4	US-09-350-259-96 Sequence 96, Appl
27	159.5	8.3	3528	1	US-08-286-889-36 Sequence 36, Appl
28	159.5	8.3	3528	1	US-08-485-618-36 Sequence 36, Appl
29	159.5	8.3	3528	1	US-08-362-652-36 Sequence 36, Appl
30	159.5	8.3	3528	1	US-08-605-672-36 Sequence 36, Appl
31	159.5	8.3	3528	2	US-08-482-293A-36 Sequence 36, Appl
32	159.5	8.3	3528	2	US-08-943-363-36 Sequence 36, Appl
33	159.5	8.3	3528	3	US-09-193-043-36 Sequence 36, Appl
34	159.5	8.3	3528	4	US-09-688-307A-36 Sequence 36, Appl
35	159.5	8.3	3528	4	US-09-350-259-36 Sequence 36, Appl
36	159.5	8.3	3597	1	US-08-485-618-54 Sequence 54, Appl
37	159.5	8.3	3597	1	US-08-362-652-54 Sequence 54, Appl
38	159.5	8.3	3597	2	US-08-605-672-54 Sequence 54, Appl
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41	159.5	8.3	3597	3	US-09-193-043-54 Sequence 54, Appl
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43	159.5	8.3	3597	4	US-09-350-259-54 Sequence 54, Appl
44	159.5	8.3	3726	1	US-08-173-497-1 Sequence 1, Appl
45	159.5	8.3	3726	1	US-08-286-889-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-833-381-998 Application US/09833381

Patent No. 6672186

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: NO. 6672186el Nucleic Acid and Protein Homologs

FILE REFERENCE: 5800-119

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 998

LENGTH: 2459

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: misc_feature

LOCATION: (1) ... (2459)

OTHER INFORMATION: n = A,T,C or G

US-09-833-381-998

Alignment Scores:

Pred. No.: 6.95e-194

Score: 1649.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 86.15%

Length: 2459

Matches: 318

Conservative: 0

Mismatches: 0

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US-09-970-076-2 (1-368) x US-09-833-381-998 (1-2459)

2/29/00 PD

9/833382

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Db 472 CTGGGCTCATCTGCGCGGAGAGGGGAGACGAGGGAGATGGGGGCTCCAGCCCTGCTAC 531
Qy 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db 532 GCGGATTTGACCTGCTTCACTTATTTGGACAATCAGAGAGTGCTGCACACCTGAGAT 591
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Qy 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db 892 TCAGAGAGGAGGCGCAATAGCTCGAGATCTTGTGCAATTGTTTACGTGGTGATG 951
Qy 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
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Qy 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
Db 1012 GTGAATGAGGCTTTCAGGCTCTGCAAGGACATCACTCAATTTTAAAGATCCCTGC 1071
Qy 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 240
Db 1072 ATCGAAATTTCTAGACGCTGAACCATCCACCAATGTGCAAGAGATCATTTCAAGTTTC 1111
Qy 241 ValArgGlyAsnGlyPheArgHisAlaIleArgAsnValAspArgValLeuCysSerPheLys 260
Db 1132 GTGAGAGGAAACGGCTTCCGACATGCCGCAACGTGACAGGGTCTCTGCAAGCTTCAAG 1191
Qy 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrIleuLeu 280
Db 1192 ATCAATGACTGGTCACTCATATGAAAGCCCTTTCTGTGAGAAAGATCTTATTACTG 1251
Qy 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db 1252 TGTCCAGGCGCTATTTAAAGAACTTGGCAATGAAAGTGCACCTCAGATGACATGAAAC 1311
Qy 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSer 318
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RESULT 2

US-09-620-312D-8

Sequence 8, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Ashundt, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Rui-hong

```

APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jiean-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghaast
APPLICANT: Drmanac, Radoye T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_Fl_genes Version 1.0
SEQ ID NO 8
LENGTH: 1609
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (309)..(1202)
US-09-620-312D-8

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Alignment Scores:

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Score: 1392.00 Matches: 267
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.26% Mismatches: 0
Query Match: 72.73% Indels: 0
DB: 4 Gaps: 0

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US-09-970-076-2 (1-368) x US-09-620-312D-8 (1-1609)

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Qy 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db 309 ATGGCCAGCGGAGGAGAGCCCTCGGACATCGGCTTCCAGTGGCTCTTTGGCCACT 368
Qy 21 LeuValLeuIleCysAlaGlyGlnGlyValArgArgIleuAspGlyIleProAlaCysTyr 40
Db 369 CTGGGCTCATCTGCGCGGAGAGGGGAGACGACAGGAGATGGGGGTCCAGCTGCTAC 428
Qy 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db 429 GCGGATTTGACCTGCTTCACTTATTTGGACAATCAGAGAGTGCTGCACACCTGAGAT 488
Qy 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
Db 489 GAAATCTATTACTTGTGAAACAGTTGGCTCACAAAATTCATCAGCCACAGTTGAGATG 548
Qy 81 SerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArgGlu 100
Db 549 TCTTTATTGTTTCTCCACCCGAGGAAACCTTAAATGAAATGAGACAGAAAGACAGAA 608
Qy 101 GlnIleArgGlnGlyLeuGlnGluGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db 609 CAAATCCCTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 668
Qy 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
Db 669 CATGAAGATTGTGAAGGGCCAGTGAAGCATTTATATGAAAACAGACAAAGGTTACAGG 728
Qy 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisIleAspLeuPhePheTyr 160
Db 729 ACAGCCAGCGTCATATTGCTTGTGACTATGAGAGAACTCCATGAAGATCTCTTTTCTAT 788

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Alignment Scores:

Pred. No.: 8,956-10 Length: 3519
 Score: 166.00 Matches: 66
 Percent Similarity: 46.15% Conservative: 42
 Best Local Similarity: 28.21% Mismatches: 96
 Query Match: 8.67% Indels: 30
 DB: 1 Gaps: 12

US-09-970-076-2 (1-368) x US-08-605-672-45 (1-3519)

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Qy 37 ProAlaCyTYrGly---GlyPheApleuTYrPheileuAaplySercIyServal 55
    |||||
Db 481 CCAAGTGTCCAGACAGACAGATGACATGCTTCTCGATGATGAGGTCCGGCAGCAT 540
    |||||
Qy 56 ---LeuHshIeTPaengluileTYrTYrPheValGluInleuAlHieIyPheile 74
    |||||
Db 541 GATCAAACTGATTCACAGATGAGAGACTTCGCAAGCTTTGATGGCCAGTTGGCG 600
    |||||
Qy 75 SerProGluInleuAArgMetSerPheileValPheSerThraArgGlyThrThleuMetlys 94
    |||||
Db 601 AGCACACACACCTCTCTCTCTGATGCAATCTCAACATCTCAAGATCTATTATACC 660
    |||||
Qy 95 LeuThraGluAArg---GluGluInleuArgGluInleuGluInleu 109
    |||||
Db 661 TTCACGGATTCACAGACAGACCTGAGCCCTGAGACCTGAGATGCATGTCAGCTC 720
    |||||
Qy 110 GlnlyValleuProGlyGlyAAspThyTYrMetHieGluGlyPheGluArgAlaSerGlu 129
    |||||
Db 721 CAA-----GGCTGACGTACACAGCCTCGGGCATCAGAAAGTGCGTGAAT 765
    |||||
Qy 130 GlnleTYrTYrGluAAspArgGlnlyTYrArgThraIa---ServalIleIleAlaIleu 148
    |||||
Db 766 GAGCATTTCTAGCAAGAAATGGGCCCCGAAAGTGCCAGAAAGATCTAATTGTCTATC 825
    |||||
Qy 149 ThrAArgGlyLeuLeuHieGluApleuPhePheTYrSerGlu---ArgGluAlaAsp 166
    |||||
Db 826 ACAAGATGGCAGAAATTCAGAGACCCCTGAGATTAACATGTCATCCCTGAACAGAG 885
    |||||
Qy 167 ArgSerAArgApleuGlyAlaIleValTYrCYValAlGlyValIyAAsp---PheAAspGlu 185
    |||||
Db 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGGGAGATCCCTCCGGGAA 936
    |||||
Qy 186 ---ThrinleuAlaArgIle-----AlaAAspSerIyAAspHieIyAlaPhe 199
    |||||
Db 937 CCCACTGCTTACAGACAGCTGAAACACATGCTGCTGCTCCCTGCGAGACCATGTCTC 996
    |||||
Qy 200 ProValAAspArgIyPheGluAlaIleuGlnlyIleIleHieSerIleuIyAAspSer 219
    |||||
Db 997 AAGGTGGGCAAT---TTGTAGCACTTCGACGATCCAGCGCAATTCAGAGAAA--- 1050
    |||||
Qy 220 CyValleGluIleLeuAlaIleAAspProSerThrinIeCYValAlGlyIySerPheGluVal 239
    |||||
Db 1051 -----ATCTTGGCATTGAGAAACCGAATCAAGGTCAAGTATCTTTTCAGACAC 1101
    |||||
Qy 240 ValValAArgGlyAAspIyPheArgHieIleAlaAAspValAAsp 253
    |||||
Db 1102 GAGATGTCAACAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143
    |||||

```

RESULT 6

US-08-605-672-45
 Sequence 45, Application US/08605672
 Patent No. 5817515
 GENERAL INFORMATION:
 APPLICANT: Gallatin, W. Michael
 APPLICANT: Van der Vieren, Monica
 TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
 NUMBER OF SEQUENCES: 103
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker Drive, 6300 Sear Tower
 CITY: Chicago
 STATE: Illinois

```

COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-605-672-45

```

Alignment Scores:

Pred. No.: 8,956-10 Length: 3519
 Score: 166.00 Matches: 66
 Percent Similarity: 46.15% Conservative: 42
 Best Local Similarity: 28.21% Mismatches: 96
 Query Match: 8.67% Indels: 30
 DB: 1 Gaps: 12

US-09-970-076-2 (1-368) x US-08-605-672-45 (1-3519)

```

Qy 37 ProAlaCyTYrGly---GlyPheApleuTYrPheileuAaplySercIyServal 55
    |||||
Db 481 CCAAGTGTCCAGACAGACAGATGACATGCTTCTCGATGATGAGGTCCGGCAGCAT 540
    |||||
Qy 56 ---LeuHshIeTPaengluileTYrTYrPheValGluInleuAlHieIyPheile 74
    |||||
Db 541 GATCAAACTGATTCACAGATGAGAGACTTCGCAAGCTTTGATGGCCAGTTGGCG 600
    |||||
Qy 75 SerProGluInleuAArgMetSerPheileValPheSerThraArgGlyThrThleuMetlys 94
    |||||
Db 601 AGCACACACACCTCTCTCTGATGCAATCTCAACATCTCAAGATCTATTATACC 660
    |||||
Qy 95 LeuThraGluAArg---GluGluInleuArgGluInleuGluInleu 109
    |||||
Db 661 TTCACGGATTCACAGACAGACCTGAGCCCTGAGACCTGAGATGCATGTCAGCTC 720
    |||||
Qy 110 GlnlyValleuProGlyGlyAAspThyTYrMetHieGluGlyPheGluArgAlaSerGlu 129
    |||||
Db 721 CAA-----GGCTGACGTACACAGCCTCGGGCATCAGAAAGTGCGTGAAT 765
    |||||
Qy 130 GlnleTYrTYrGluAAspArgGlnlyTYrArgThraIa---ServalIleIleAlaIleu 148
    |||||
Db 766 GAGCATTTCTAGCAAGAAATGGGCCCCGAAAGTGCCAGAAAGATCTAATTGTCTATC 825
    |||||

```

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QY 149 ThisArgLgUgUleNhiGSLuAryLeuherhEtyrserGlu-----ArgLgUlaAyn 166
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 826 AACAGTGGGACCAAAATTCAGAAACACCCCTGGAGATAGACATGTATGCTCTGAAACAGAG 885
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 167 ArgSerAaGAArLeuGluYAlaIleValTyrCySValGluYValuAaP---PheAaGlu 185
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 886 AAAGCT-----GGGATCATCTGCGATGTATAGGGGGGTGGAGATGCTTCGGGAA 936
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 186 ---ThrGlnLeuAlaArgIle-----AlaSerSerLysAaPhtIValPhe 199
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 937 CCCAGTGGCCCTACAGAGCTGAACACCATTTGGCTCAGCTCCCTCCAGACACACACGCTTTC 996
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 200 ProValaAaAaerGlyPheGlnAlaLeuGlnGluIleIleHisSerIleLeuLysPsser 219
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 997 AAGGTGGGCACAT---TTTGTACACTTTCGACACTTCAGACATCCAGCGCAATTCAGAGAAA--- 1055
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 CySileGluIleLeuAlaAlaGluProSerThrIleCySValGluLysPheGlnVal 239
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1051 -----ATCTTTGGCATTTGAAGAAACCGAATCAAGTAAAGTATCTTTTCAGCAC 1101
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 ValValaArgGlyAaGluPheArgGlnValAaGaaValaAaP 253
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1102 GAGATGTCAACAGAAAGTTTTCAGCTCAGCTCTCTCAATGGAT 1143
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-08-482-293A--45
; Sequence 45, Application US/08482293A
; Patent No. 5831029
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,293A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27666/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

[illegible]


```

CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-943-363-45

Alignment Scores:
Pred. No.: 8.95e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-2 (1-368) x US-08-943-363-45 (1-3519)
QY 37 ProAlaCytyrGly---GlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerVal 55
DB 481 CCAAGAGTGTCCAGCAAGAGATGACATGCTTCTGATGATGATGCTCCGCGAGCAT 540
QY 56 ---LeuHleHleTrpLeuGluLeuTyrrTyrrPheValGluGluLeuAlaHleIshPheIle 74
DB 541 GATCAAGAGATTTTACCAAGATGAAGACTTCCTCAAGACTTTGATGGCCAGATTGGG 600
QY 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
DB 601 ACCACACAGACCTCGTCTCTGATGCAATGACTCAACATCTGGAAGACTCATTTACC 660
QY 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 109
DB 661 TTCACGGAATTCAAGACGAGCTGAGCCCTCAGAGCTGTGAGATGCCATCGTCCAGTC 720
QY 110 GlnLysValLeuProGlyGlyAspThrTyrrMetHleGluGlyPheGluArgAlaSerGlu 129

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DB 721 CAA-----GGCTGACGTACACAGCTTCGGGCATCCAGAAAGTGTGAA 765
QY 130 GlnIleTyrrGluAsnArgGlnGlyTyrrArGthrAla-----SerValIleIleAlaLeu 148
DB 766 GAGTATTTTCATGACAGAAATGGGGCCGAAAGATGCCAAGAAATCTAATTGTCAATC 825
QY 149 ThrAspGlyLeuHleGluLeuPhePheTyrrSerGlu-----ArgGluAlaAsn 166
DB 826 ACAGATGGCAGAAATTCAGAGACCCCTGAGATTAACATGTCATCCCTGAAGACAG 885
QY 167 ArgSerArgAspLeuGlyAlaIleValTyrrCyValGlyValLysAsp---PheAsnGlu 185
DB 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCCCTCCGGGAA 936
QY 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199
DB 937 CCCACTGCCCTTACAGAGACTAACCATTGGCTTCAGCTCCCTCGAGAGCCACCTGTTC 996
QY 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHleIshSerIleLeuLysSer 219
DB 997 AAGGTGGGCAT---TTGTAGCACTTTCGACATCCAGCGGCAATTCCAGAGAAA--- 1050
QY 220 CysIleGluIleLeuAlaIleGluProSerThrIleCyAlaGlyGluSerPheGlnVal 239
DB 1051 -----ATCTTGGCCATTGAAGAACCGAATCAAGGTGTTCCCTTCAGCAC 1101
QY 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253
DB 1102 GAGATGTCACAAAGAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 9
US-09-193-043-45
Sequence 45, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45
LENGTH: 3519
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(3516)
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-193-043-45

Alignment Scores:
Pred. No.: 8.95e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 3 Gaps: 12

US-09-970-076-2 (1-368) x US-09-193-043-45 (1-3519)
QY 37 ProAlaCytyrGly---GlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerVal 55

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Db      481  CCAGAGTGTCCAGGACAAAGAGATGACATGTGCTTCCGATGATGAGGCTCCGGACGACTT 540
Oy      56  ---LeuHsiHstrpaEngIuileTyrrPhreValGluGlnLeuAlaHieLysPhe1le 74
Db      541  GATCAAAATGACTTATCCCAATGAAGAGCTTGGTCAAAAGCTTGTATGAGGCGAGTGGCG 600
Oy      75  SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThreLys 94
Db      601  AGCACCAGACACCTGCTCTCCCTGATGCAATATCAACATCTGTAAGACTCATTTTACC 660
Oy      95  LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 109
Db      661  TTCACGAAATTCACAGACAGCCTGAGCCCTGAGACCTCGGTGATGCGATGCTGCAGCTC 720
Oy      110  GlnLysValLeuProGlyGlyValPheThrTyrrMetHieGluGlyPheGluArgAlaSerGlu 129
Db      721  CAA-----GGCTGACGTACACAGCCTGGGCGATCCAAAGATGGTGAA 765
Oy      130  GlnIleTyrrGluAsnArgGlnGlyTyrrArgThrAla---SerValIleIleAlaLeu 148
Db      766  GAGTATATTCATACAGAAATGAGGCGCCGAAAAGTCCCAAGAAATATCTATTTGTATC 825
Oy      149  ThrArgGlyGluLeuHieGluAspLeuPhePheTyrrSerGlu-----ArgGluAlaAsn 166
Db      826  ACAGATGGGCAAAATTCAGAGACCCCTGAGATGACATGTCTATCCTGAAAGCAGAG 885
Oy      167  ArgSerArgAspLeuGlyAlaIleValTyrrCysValGlyValLysAsp---PheAsnGlu 185
Db      886  AAGCT-----GGATCATTTGGCTATGCTATAGGGGTGGAGATGCTCCGGGAA 936
Oy      186  ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHieValPhe 199
Db      937  CCCACTGCCCTACAGAGCTGAACACATGTGGCTCAGCTCCCTCCGACAGACACGCTGTC 996
Oy      200  ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHieSerIleLeuLysSer 219
Db      997  AAGGTGGCAAT---TTGTAGCACTTCGACAGCATCCGCGCAATTCAGAGAA--- 1050
Oy      220  CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysPheGlnVal 239
Db      1051  -----ATCTTTGCCATTGAAAGAACCAATCAAGCTCAATGATCTCTTCAGAC 1101
Oy      240  ValValArgGlyAsnGlyPheArgHieValArgAsnValAsp 253
Db      1102  GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 10
US-09-688-307A-45
; Sequence 45, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688.307A
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193.043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605.672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173.497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286.889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362.652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943.363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45

```

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; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

Alignment Scores:
Pred. No.:      8.95e-10      Length:      3519
Score:          166.00      Matches:      66
Percent Similarity: 46.15%      Conservative: 42
Best Local Similarity: 28.21%      Mismatches: 30
Query Match:      8.67%      Indels:      96
DB:               4          Gaps:      12

US-09-970-076-2 (1-368) x US-09-688-307A-45 (1-3519)

Oy      37  ProAlaCysTyrrGly---GlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerVal 55
Db      481  CCAGAGTGTCCAGGACAAAGAGATGACATGTGCTTCCGATGATGAGGCTCCGGACGACTT 540
Oy      56  ---LeuHsiHstrpaEngIuileTyrrPhreValGluGlnLeuAlaHieLysPhe1le 74
Db      541  GATCAAAATGACTTATCCCAATGAAGAGCTTGGTCAAAAGCTTGTATGAGGCGAGTGGCG 600
Oy      75  SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThreLys 94
Db      601  AGCACCAGACACCTGCTCTCCCTGATGCAATATCAACATCTGTAAGACTCATTTTACC 660
Oy      95  LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 109
Db      661  TTCACGAAATTCACAGACAGCCTGAGCCCTGAGACCTCGGTGATGCGATGCTGCAGCTC 720
Oy      110  GlnLysValLeuProGlyGlyValPheThrTyrrMetHieGluGlyPheGluArgAlaSerGlu 129
Db      721  CAA-----GGCTGACGTACACAGCCTGGGCGATCCAAAGATGGTGAA 765
Oy      130  GlnIleTyrrGluAsnArgGlnGlyTyrrArgThrAla---SerValIleIleAlaLeu 148
Db      766  GAGTATATTCATACAGAAATGAGGCGCCGAAAAGTCCCAAGAAATATCTATTTGTATC 825
Oy      149  ThrArgGlyGluLeuHieGluAspLeuPhePheTyrrSerGlu-----ArgGluAlaAsn 166
Db      826  ACAGATGGGCAAAATTCAGAGACCCCTGAGATGACATGTCTATCCTGAAAGCAGAG 885
Oy      167  ArgSerArgAspLeuGlyAlaIleValTyrrCysValGlyValLysAsp---PheAsnGlu 185
Db      886  AAGCT-----GGATCATTTGGCTATGCTATAGGGGTGGAGATGCTCCGGGAA 936
Oy      186  ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHieValPhe 199
Db      937  CCCACTGCCCTACAGAGCTGAACACATGTGGCTCAGCTCCCTCCGACAGACACGCTGTC 996
Oy      200  ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHieSerIleLeuLysSer 219
Db      997  AAGGTGGCAAT---TTGTAGCACTTCGACAGCATCCGCGCAATTCAGAGAA--- 1050
Oy      220  CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysPheGlnVal 239
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Oy      240  ValValArgGlyAsnGlyPheArgHieValArgAsnValAsp 253
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RESULT 11
US-09-350-259-45
; Sequence 45, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.

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APPLICANT: Van der Vieren, Monica
 TITLE OF INVENTION: No. 662091561 Human 2
 FILE REFERENCE: 27866/35004
 CURRENT APPLICATION NUMBER: US/09/350,259
 CURRENT FILING DATE: 1999-07-08
 EARLIER APPLICATION NUMBER: 09/193,043
 EARLIER FILING DATE: 1998-11-16
 EARLIER APPLICATION NUMBER: 08/173,497
 EARLIER FILING DATE: 1993-12-23
 EARLIER APPLICATION NUMBER: 08/286,889
 EARLIER FILING DATE: 1994-08-05
 EARLIER APPLICATION NUMBER: 08/362,652
 EARLIER FILING DATE: 1994-12-21
 EARLIER APPLICATION NUMBER: 08/943,363
 EARLIER FILING DATE: 1997-10-03
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 45
 LENGTH: 3519
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (52)..(3516)
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: primer
 US-09-350-259-45

Alignment Scores:
 Pred. No.: 8,95e-10 Length: 3519
 Score: 166.00 Matches: 66
 Percent Similarity: 46.15% Conservative: 42
 Best Local Similarity: 28.21% Mismatches: 96
 Query Match: 8.67% Indels: 30
 DB: Gaps: 12

US-09-970-076-2 (1-368) x US-09-350-259-45 (1-3519)

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 56 ---LeuHhHtRpaAenGluIleuTyRrPhaValGluInleuAlaHleuSphelle 74
 541 GATCAAGTGAATTAACCAAGATGAAGAGCTTCGCAAGCTTATGAGCCAGTTGGC 600
 75 SerProGluLeuArgMetSerPheIleValPheSerThrArgGlyThrThreMetLys 94
 601 AGCACCAGACCTCGTCTCCTGATGCAATACTCAACATCTCGAAGACTCATTTTACC 660
 95 LeuThrGluAparG---GluGlnIleArgGlnGlyLeuGluGluLeu 109
 661 TTCACGGAATTCAGAGCAGCTGAGCCCTGAGCCTGAGATGATGATGATGATGATG 720
 110 GlnLysValLeuPrgGlyGlyAspThrTyMetHleGluGlyPheGluArgLaserGlu 129
 721 CAH-----GAGCTGAGTACACAGCTCGGAGCATCCAGAAATGCTGAAA 765
 130 GlnIleTyRrGluAsnArgGlnGlyTyArgThrAla---SerValIleIleAlaLeu 148
 766 GAGCATTTTCATGACAAAGATGGGCGGAAAGATGCAAGATATCTATTTGTCATC 825
 149 ThrArgGlyGluLeuHleGluApleuPhePheTySerGlu-----ArgGluAlaAsn 166
 826 ACAGATGGCGCAAAATTCAGAGACCCCTGAGATGATGACATGATGATGATGATGATG 885
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 886 AAGCT-----GGATCATTTGCTATGAGGATGAGGATGAGGATGAGGATGAGGAT 936
 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199
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 997 AAGTGGGAGCAT---TTTGTGACACTTCGAGCATCCAGCGCAATTCAGAGAAA--- 1050
 220 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 239
 1051 -----ATCTTGGCATTTGAAGAACCAATCAAGTCAAGTATGTTCTTCACGAC 1101
 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253
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 US-08-485-618-52
 Sequence 52, Application US/08485618
 Patent No. 5728533
 GENERAL INFORMATION:
 APPLICANT: Gallatin, W. Michael
 APPLICANT: Van der Vieren, Monica
 TITLE OF INVENTION: No. 572853361 Human 2 Integrin Alpha Subunit
 NUMBER OF SEQUENCES: 103
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
 STREET: 233 South Wacker Drive, 6300 Seear Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,618
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/173,497
 FILING DATE: 23-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,889
 FILING DATE: 5-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/362,652
 FILING DATE: 21-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams Jr., Joseph A.
 REGISTRATION NUMBER: 38,659
 REFERENCE/DOCKET NUMBER: 27866/32797
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3803 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3486
 US-08-485-618-52
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 Pred. No.: 1.02e-09 Length: 3803
 Score: 166.00 Matches: 66
 Percent Similarity: 46.15% Conservative: 42
 Best Local Similarity: 28.21% Mismatches: 96
 Query Match: 8.67% Indels: 30

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SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 3803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3486
US-08-482-293A-52

Alignment Scores:
Pred. No.: 1.02e-09 Length: 3803
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
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DB 480 GATCAAAGTGAATTACCAAGATGAAGACTTCGTCAAAGCTTTGATGGCCAGTGGCG 549
QY 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
DB 550 AGCACACAGACACTCGTCTCTCCCTGATGCAATCTCAACATCTGAAGATCATTTTACC 609
QY 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 109
DB 610 TTCACGGAATTCAGAGCAGCTGAGCCCTGAGCCCTGAGCTGATGATGATGATGATGATG 669
QY 110 GlnLysValLeuProGlyGlyAspThrTyrMetH1eGluGlyPheGluArgAlaSerGlu 129
DB 670 CAA-----GGCTGACGTCACACAGCTCGGCGATCCAGAAATGTGTGAA 714
QY 130 GlnIleTyrTyrGluAspArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeu 148
DB 715 GAGCATATTTCATACGAAGAATGGGCGCGAAAGATGCGCAAGAGATATCTAATTGTATC 774
QY 149 ThrAspGlyGluLeuH1eGlnAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 166
DB 775 ACAGATGGGCGAAGAAATTCAGAGACCCCTGAGTATAGACATGTCATCCCTGAAGCAGAG 834

QY 167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu 185
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QY 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspH1eValPhe 199
DB 886 CCACTCCCTTACAGAGCTGAACACATTCGCTCAGCTCCCTGCGAGACACGTGTT 945
QY 200 ProValAspArgGlyPheGlnAlaLeuGlnGlyIleIleH1eSerIleLeuLysSer 219
DB 946 AAGGTGGCAAT---TTGTAGACATTCGACGATCCAGCGCGCAATTCAGAGAA--- 999
QY 220 CysIleGluIleLeuAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 239
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QY 240 ValValArgGlyAsnGlyPheArgH1eAlaArgAsnValAsp 253
DB 1051 GAGATGTCAAGAAAGGTTTCAGCTCAGCTCTCTCAATGAT 1092

Search completed: June 22, 2004, 02:52:35
Job time : 95.151 secs

GenCore version 5.1.6
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Run on: June 22, 2004, 01:18:40 ; Search time 72.528 Seconds
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Title: US-09-970-076-8

Perfect score: 1728
Sequence: 1 MATERRALGIGFOWLSLAT.....TTHCSLHKIAGPTTAACME 333

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Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :

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6: /cg2_6/pdata/2/1na/Backfiles1.seg:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1728	100.0	2459	4	US-09-833-381-998 Sequence 998, App
2	1392	80.6	1609	4	US-09-620-312D-8 Sequence 8, Appl
3	166	9.6	3519	1	US-08-286-889-45 Sequence 45, Appl
4	166	9.6	3519	1	US-08-485-618-45 Sequence 45, Appl
5	166	9.6	3519	1	US-08-362-652-45 Sequence 45, Appl
6	166	9.6	3519	1	US-08-605-672-45 Sequence 45, Appl
7	166	9.6	3519	2	US-08-482-293A-45 Sequence 45, Appl
8	166	9.6	3519	2	US-08-943-363-45 Sequence 45, Appl
9	166	9.6	3519	3	US-09-193-043-45 Sequence 45, Appl
10	166	9.6	3519	4	US-09-688-307A-52 Sequence 52, Appl
11	166	9.6	3519	4	US-09-350-259-54 Sequence 54, Appl
12	166	9.6	3803	1	US-08-485-618-52 Sequence 52, Appl

13	166	9.6	3803	1	US-08-362-652-52 Sequence 52, Appl
14	166	9.6	3803	1	US-08-605-672-52 Sequence 52, Appl
15	166	9.6	3803	2	US-08-482-293A-52 Sequence 52, Appl
16	166	9.6	3803	3	US-08-943-363-52 Sequence 52, Appl
17	166	9.6	3803	4	US-09-193-043-52 Sequence 52, Appl
18	166	9.6	3803	4	US-09-688-307A-52 Sequence 52, Appl
19	166	9.6	3803	4	US-09-350-259-52 Sequence 52, Appl
20	159.5	9.2	2499	1	US-08-485-618-96 Sequence 96, Appl
21	159.5	9.2	2499	1	US-08-605-672-96 Sequence 96, Appl
22	159.5	9.2	2499	2	US-08-482-293A-96 Sequence 96, Appl
23	159.5	9.2	2499	2	US-08-943-363-96 Sequence 96, Appl
24	159.5	9.2	2499	3	US-09-193-043-96 Sequence 96, Appl
25	159.5	9.2	2499	3	US-09-688-307A-96 Sequence 96, Appl
26	159.5	9.2	2499	4	US-09-350-259-96 Sequence 96, Appl
27	159.5	9.2	3528	1	US-08-286-889-36 Sequence 36, Appl
28	159.5	9.2	3528	1	US-08-485-618-36 Sequence 36, Appl
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31	159.5	9.2	3528	2	US-08-482-293A-36 Sequence 36, Appl
32	159.5	9.2	3528	2	US-08-943-363-36 Sequence 36, Appl
33	159.5	9.2	3528	3	US-09-193-043-36 Sequence 36, Appl
34	159.5	9.2	3528	4	US-09-688-307A-36 Sequence 36, Appl
35	159.5	9.2	3528	4	US-09-350-259-36 Sequence 36, Appl
36	159.5	9.2	3597	1	US-08-485-618-54 Sequence 54, Appl
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39	159.5	9.2	3597	2	US-08-482-293A-54 Sequence 54, Appl
40	159.5	9.2	3597	2	US-08-943-363-54 Sequence 54, Appl
41	159.5	9.2	3597	3	US-09-193-043-54 Sequence 54, Appl
42	159.5	9.2	3597	4	US-09-688-307A-54 Sequence 54, Appl
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44	159.5	9.2	3726	1	US-08-173-497-1 Sequence 1, Appl
45	159.5	9.2	3726	1	US-08-286-889-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-833-381-998
; Sequence 998, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833, 381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FASTSeq for Windows Version 3.0
; SEQ ID NO 998
; LENGTH: 2459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (2459)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-998

Alignment Scores:

Pred. No.: 2.79e-213 Length: 2459
Score: 1728.00 Matches: 333
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-8 (1-333) x US-09-833-381-998 (1-2459)

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Db      472 CTGGTGCTCATTCGGCCGGGCGAGGGGAGCCAGAGAGATGGGGGTCCAGCTGCTAC 531
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Db      532 GCGCGATTGACCTGTACTTCATTTTGGACAAATCAGAGAGTGCTGTCCACACATCGAAT 591
Qy      61  GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlyLeuAspMet 80
Db      592 GAAATCTATTACTTGTGGACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAAG 651
Qy      81  SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
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Qy      101  GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
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Qy      141  ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160
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Qy      161  SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db      892 TCAGAGAGGAGAGGCTAATAGGCTCTGAGATCTTGGTGAATGTTTACGTGGTGGTGTG 951
Qy      892  LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
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Qy      201  ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
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APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Weinman, Tom
APPLICANT: Xue, Aildong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radjoje T.
TITLE OF INVENTION: No. 6596262el Nucleic Acids and
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 8
LENGTH: 1609
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (309)..(1202)
US-09-620-312D-8
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Qy      61  GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuAspMet 80
Db      489  GAAATCTATTACTTGTGGACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAAG 548
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QY 141 ThrAlaSerValIleIleAlaLeuThraPheArgLYGluLeuHieGluAerPhePheTyr 160
 DB 729 ACAAGCAGGTCATCATCTTCTTGAATGAGAACTCCAGAAATCTCTTTTCTAT 788
 QY 161 SerGluArgGluAlaAsnArgSerArgAerPheGluAlaIleValTyrCyValGlyVal 180
 DB 789 TCAGAGAGGAGGATTAATGATCTCGAGATCTTGCGCAATGTTACTGCTTGCTGGTG 848
 QY 181 LysAerPheAsnGluThrGluLeuAlaArgIleAlaAerSerLysAerHisValPhePro 200
 DB 849 AAAGATTCCTATGAGACACAGCTGGCCCGAATGCGGACAGTAAGATCATGTGTTTCCC 908
 QY 201 ValAAsnArgGlyPheGluAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
 DB 909 GCGAATGACGGCTTTCAGGCTCTCGAAGGCATCATCTCAATTTTGAAGAAGTCTTCC 968
 QY 221 IleguIleLeuAlaAlaGluProSerThrIleCyValGlyGluSerPheGlnValVal 240
 DB 969 ATCGAAATCTTAGCAGCTGACCATTCACCATATGTCGAGAGAGTCATTTCAGTTGTC 1028
 QY 241 ValAArgGlyAAsnGlyPheArgHisAlaAerAAsnValAerArgValLeuCySerPheLys 260
 DB 1029 GCGAAGGAAACGGCTTCGACATGCCGCAACGTGACAGGCTCCTCGACGTTTCAAG 1088
 QY 261 IleAAsnArgSerValThrLeuAAsnGlu 269
 DB 1089 ATCAATGACTCGCTCACACTCAGTAAAG 1115

RESULT 3

US-08-286-889-45
 ; Sequence 45, Application US/08286889
 ; Patent No. 5470953
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Mich
 ; APPLICANT: Van der Vieren, Monica
 ; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive, 6300 Seear Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/286,889
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/173,497
 ; FILING DATE: 23-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Williams Jr., Joseph A.
 ; REGISTRATION NUMBER: P38,659
 ; REFERENCE/DOCKET NUMBER: 27866/32168
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3519 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS

; LOCATION: 52..3519
 ; US-08-286-889-45
 Alignment Scores:
 Pred. No.: 1.29e-10 Length: 3519
 Score: 166.00 Matches: 66
 Percent Similarity: 46.15% Conservative: 42
 Best Local Similarity: 28.21% Mismatches: 96
 Query Match: 9.61% Indels: 30
 DB: 1 Gaps: 12

US-09-970-076-8 (1-333) x US-08-286-889-45 (1-3519)

QY 37 ProAlaCysTyrGly---GlyPheAsnLeuTyrPheIleLeuAerPheLysSerVal 55
 DB 481 CCAAGTCTCCAGGACCAAGAATGACATGCTTCTCGATGATGAGCTCCGAGCATTT 540
 QY 56 ---LeuHisIleStrPAsnGluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIle 74
 DB 541 GATCAAAAGTGACTTTAACCCAGATGAAGGACTTCGTCAAGCTTTGATGGGCAATTGGCG 600
 QY 75 SerProGlnLeuAerGluMetSerPheIleValPheSerThrArgGlyThrThiLeuMetLys 94
 DB 601 AGCACACACACCTGCTCTCCCTGATGCAATATCAACATCTGAACTGATTTTACC 660
 QY 95 LeuThrGluAerArg-----GluGlnIleArgGlnGlyLeuGlnGlu 109
 DB 661 TTCACGGAAATTCAGACAGACGCTTACGCTTACGAGCTGTTGATGCCATGCTCCAGCTC 720
 QY 110 GlnLysValLeuProGlyGlyAerThrTyrMetHisGlnGlyPheGluArgAAsnGlu 129
 DB 721 CAA-----GGCTGACGTACACAGCTCGGGCATTCAGAAAGTGATGA 765
 QY 130 GlnIleTyrTyrGluAAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeu 148
 DB 766 GAGCATTTCTATGACAAAGATGGGCGCCGCAAAAGTCCCAAGAAATATCTAATGTCTATC 825
 QY 149 ThrAerGlyGluLeuHisGluAAsnLeuPhePheTyrSerGlu-----ArgGluAAsn 166
 DB 826 ACAAGTGGGCAAAATTCAGAAACCCCTGAGATGTAGACATGTGATCCCTGAAACCAAG 885
 QY 167 ArgSerArgAerPheGluAlaIleValTyrCyValGlyValLysAer---PheAAsnGlu 185
 DB 886 AAAGCT-----GGATCATTTGCTATGTCTATAGGGGTGGAGATGCTTCGGGGA 936
 QY 186 ---ThrGlnLeuAlaArgIle-----AlaAerSerLysAerHisValPhe 199
 DB 937 CCCACTGCCCTTACAGAGACTGAAACACATTTGGCTCAGCTCCCTCGACAGACACGTTTC 996
 QY 200 ProValAAsnArgGlyPheGlnAlaLeuGlnGlnGlyIleIleHisSerIleLeuLysSer 219
 DB 997 AAGGTGGGCAT---TTTGTAGCACTTGCAGCATCCAGCGCAAAATTCAGAGAA--- 1050
 QY 220 CysIleguIleLeuAlaAlaGluProSerThrIleIleHisSerIleLeuLysSerPheGlnVal 239
 DB 1051 -----ATCTTGGCATTTGAAGAAACCAATCAAGTCAAGTTCCTTTCAAGCAC 1101
 QY 240 ValValAArgGlyAAsnGlyPheArgHisAlaAerAAsnValAer 253
 DB 1102 GAGATGCACAAAGAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 4

US-08-485-618-45
 ; Sequence 45, Application US/08485618
 ; Patent No. 5728533
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Van der Vieren, Monica
 ; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
 ; NUMBER OF SEQUENCES: 103
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive, 6300 Seear Tower

CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-485-618-45

Alignment Scores:
Pred. No.: 1,296-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 9.61% Indels: 30
Gaps: 12

US-09-970-076-8 (1-333) x US-08-485-618-45 (1-3519)

QY 37 ProAlaCyGTYTGly---GlyPheAspLeuTYrPheIleLeuAspLysSerGlySerVal 55
DB 481 CGAGGTGTCCAGGCAAGAGATGACATGCTTCTTCGATGATGAGGCTCCGGCGACGACTT 540
QY 56 ---LeuH18H18TRAsnglnu1eTYrTYrPheValGlnGlnLeuAlaH18LysPheIle 74
DB 541 GATCAAGTGAATTAACCAAGATGAAGACTTCGCAAGCTTATATGGCCAGTTGGCG 600
QY 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThreLeuMetLys 94
DB 601 AGCACGACGACCTGCTTCTCCGATGCAATCTCAAAACATCTTAAGATCATTTTACC 660
QY 95 LeuThrglnAspArg-----GlnGlnIleArgGlnGlyLeuGlnGlnLeu 109
DB 661 TTCACGGAATTCAGACGACCTGAGCCCTGAGCCCTGAGCTGATGCATGTCACGCTC 720
QY 110 GlnLysValLeuProGlyGlyAspThrTYrMetH18GlnGlyPheGlnArgAlaSerGlu 129
DB 721 CAA-----GGCTGACGTACACAGCCTCGGAGCATCCAGAAAGTGTGAAA 765
QY 130 GlnIleTYrTYrGlnAsnArgGlnGlyTYrArgThrAla---SerValIleIleAlaLeu 148

DB 766 GAGCTATTTCATAGCAAGAAATGGGCCCCGAAAAAGTCCAAAGAAATACTAATTGTGATC 825
QY 149 ThrAspGlyGlnLeuH18GlnAspLeuPhePheTYrSerGlu-----ArgGlnAlaAsn 166
DB 826 ACAGATGGGCAAGAAATTCAGAGACCCCTGGAGTATGACATGTCATCCCTGAAGCAGAG 885
QY 167 ArgSerArgAspLeuGlnAlaIleValTYrCysValGlyValLysAsp---PheAsnGlu 185
DB 886 AAAGCT-----GGGATCATTGCGCTATGCTATAGGGGTGGAGATGCTTCGGGGA 936
QY 186 ---ThrglnLeuAlaArgIle-----AlaAspSerLysAspH18ValPhe 199
DB 937 CCCAGTCCCTTACGAGAGCTGAACACCATTTGGCTCAGCTCCCTGCAAGACGATGTC 996
QY 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleH18SerIleLeuLysSer 219
DB 997 AAGGTGGGCAAT---TTGTAGCATTTGACGAGCATCCAGCGGCAAAATTCAGAGAAA-- 1050
QY 220 CysIleGlnIleLeuAlaIaGlnProSerThrIleCysAlaGlyLysSerPheGlnVal 239
DB 1051 -----ATCTTGCCATTGAAGAGAACCGAATCAAGGTCACTAGTCTTTCAGCAC 1101
QY 240 ValValArgGlyAsnGlyPheArgH18AlaArgAsnValAsp 253
DB 1102 GAGATGTCACAAAGAGTTTCAGCTCAGCTCTCTCATGTAT 1143

RESULT 5
US-08-362-652-45
Sequence 45, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA


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Qy 130 GlnIleTyTyrGluAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaIleu 148
      ::::::::::: ::::::::::: :::::::::::
Db 766 GAGCATTTCTATAGCAAGATGGGGCCGAAAAGTCCAGAGATCTATTATGTGATC 825
Qy 149 ThrArgGlyGluLeuHisGluAspLeuPhePheTyrSerGlu----ArgGluAlaAsn 166
      ::::::::::: ::::::::::: :::::::::::
Db 826 ACAAGTGGCGCAAAATTCCAGACCCCTGGAGTATACATGTCATCCCTGGAAGCAGAG 885
Qy 167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValAsp---PheAsnGlu 185
      ::::::::::: ::::::::::: :::::::::::
Db 886 AAAGCT-----GGAGTCAITTCGCTATGCTATAGGGAGGAGATGCTTCGGGAA 936
Qy 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerTyrAspHisValPhe 199
      ::::::::::: ::::::::::: :::::::::::
Db 937 CCCACTGCCCTTACAGAGAGCTGAACCATGTGGCTCAGCTCCCTCGCAGACCACTGTTC 996
Qy 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 219
      ::::::::::: ::::::::::: :::::::::::
Db 997 AAGGTGGGCAAT---TTGTAGCACTTCGACATCCAGCGCAAAATTCAGAGAAA--- 1050
Qy 220 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGluVal 239
      ::::::::::: ::::::::::: :::::::::::
Db 1051 -----ATCTTGGCATTGAAAGAACCGAATCAAGCTCAAGTAGTTCCTTCAGACAC 1101
Qy 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253
      ::::::::::: :::::::::::
Db 1102 GAGATGTCACAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

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RESULT 7

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US-08-482-293A-45
; Sequence 45, Application US/08482293A
; Patent No. 5831029

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GENERAL INFORMATION:

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; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402

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COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,293A
; FILING DATE:

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CLASSIFICATION: 530

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994

```

PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448

```

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; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:

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; SEQUENCE CHARACTERISTICS:

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; LENGTH: 3519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..3519
; US-08-482-293A-45

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Alignment Scores:

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Pred. No.: 1.29e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 9.61% Indels: 30
DB: Gaps: 12

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US-09-970-076-8 (1-333) x US-08-482-293A-45 (1-3519)

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Qy 37 ProHlaCysTyrGly---GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerVal 55
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 CCAGAGTGTCCAGACAGAGATGACATGCTTCTCTGATGATGCTCCGACGACATT 540
Qy 56 ---LeuHisIleTrpAsnGluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIle 74
      ::::::::::: ::::::::::: :::::::::::
Db 541 GATCAAGTAGACTTACCCAGATGAAGACCTCGTCAAGCTTTGATGGCGGCGGCG 600
Qy 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrIleuMetLys 94
      ::::::::::: ::::::::::: :::::::::::
Db 601 AGCACAGACACTTCCTCTCTGATGCAATCTCAAAACATCTGAAGACTATTATACC 660
Qy 95 LeuThrIleAspArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 109
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 TTCACGGAATTCAGAGACACCTGAGCCCTCAGAGCTGTGATGCTATGCTTCACGCTC 720
Qy 110 GlnLysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGlu 129
      ::::::::::: ::::::::::: :::::::::::
Db 721 CAA-----GGCTGACGTACACAGCTCGGGGCAATCCAGAAAGTGTGAAA 765
Qy 130 GlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaIleu 148
      ::::::::::: ::::::::::: :::::::::::
Db 766 GAGCTATTTCAATGACAAAGATGGGGCCGAAAAGTCCAAAGATATCTAATTTGTGATC 825
Qy 149 ThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu----ArgGluAlaAsn 166
      ::::::::::: ::::::::::: :::::::::::
Db 826 ACAAGTGGCGCAAAATTCCAGACCCCTGGAGTATACATGTCATCCCTGGAAGCAGAG 885
Qy 167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValAsp---PheAsnGlu 185
      ::::::::::: ::::::::::: :::::::::::
Db 886 AAAGCT-----GGAGTCAITTCGCTATGCTATAGGGAGGAGATGCTTCGGGAA 936
Qy 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerTyrAspHisValPhe 199
      ::::::::::: ::::::::::: :::::::::::
Db 937 CCCACTGCCCTTACAGAGAGCTGAACCATGTGGCTCAGCTCCCTCGCAGACCACTGTTC 996
Qy 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 219
      ::::::::::: ::::::::::: :::::::::::
Db 997 AAGGTGGGCAAT---TTGTAGCACTTCGACATCCAGCGCAAAATTCAGAGAAA--- 1050
Qy 220 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGluVal 239
      ::::::::::: ::::::::::: :::::::::::
Db 1051 -----ATCTTGGCATTGAAAGAACCGAATCAAGCTCAAGTAGTTCCTTCAGACAC 1101
Qy 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253
      ::::::::::: :::::::::::
Db 1102 GAGATGTCACAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

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RESULT 8

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US-08-943-363-45
; Sequence 45, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:

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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 58374781 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-943-363-45
Alignment Scores:
Pred. No.: 1,296-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 9.61% Indels: 30
DB: 2 Gaps: 12
US-09-970-076-8 (1-333) x US-08-943-363-45 (1-3519)
QY 37 ProAlaCybTyrgLy---GlypheAspLeuTyrrPheileLeuAspLyseSerLyseVal 55
DB 481 CCAAGGTGTCCAGACAGAGATGACATGCTTCCCTGATGATGCGTCCGCGACGACTT 540
QY 56 ---LeuHhNHtGrpAbngLuleTyrrTyrrPheValGluGlnLeuAlHhLeYarPheile 74
DB 541 GATCAAGTACTTACCAAGATGAAAGACTTCGTCAAGCTTGTATGGCCAGTTGGCG 600
QY 75 SerProGlnLeuArxMetSerPheileValPheSerThrArgLyThrThrLeuMetLys 94
DB 601 AGCACCAGACCTCTTCTCCCTGATGCAATCTCAACATCTGAAGACTCATTTTACC 660
QY 95 LeuThrgLueAspArg-----GluGlnIleArgGlnGlyLeuGlnLueu 109

DB 661 TTCAAGAAATTCAGAGACGCTGAGCCCTGACAGCTGTGTGATGCCATGCTCCAGCTC 720
QY 110 GlnYsValLeuProGlyLyAspThrTyrrMetHsGlnGlyPheGluArxAlaSerGlu 129
DB 721 CAA-----GgCCTGCGTACAGAGCTCGGGGATCCAGAAAGTGTGAA 765
QY 130 GlnIleTyrrGluAsnArgGlnGlyTyrrArgThrAla---SerValIleLeuAlaLeu 148
DB 766 GAGCATTTTCATAGCAAGATGGGGCCCGGAAAAGTGCCAGAAAGATCTAATTCATC 825
QY 149 ThrAspGlyGluLeuHsGluAspLeuPhePheTyrrSerGlu----ArgGluAlaAsn 166
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGAGATATACATGTCATCCCTGAAGACAG 885
QY 167 ArgSerArgAspLeuGlyAlaIleValTyrrCySValGlyValYAsp---PheAsnGlu 185
DB 886 AAAGCT-----GGATCATTCGTATGCTATAGGGGGGAGATGCTTCGGGAA 936
QY 186 ---ThrgInLeuAlaArgIle-----AlaAspSerLyAspHsValPhe 199
DB 937 CCCACTGCCCTTACAGAGACTGAACACATGGCTCAGCTCCCTCGACAGACCACTGTC 996
QY 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHsSerIleLeuLyAspSer 219
DB 997 AAGTGGGCAAT---TTGTAGCACTTCGACAGATCCAGCGCAAAATTCAGAGAAA--- 1050
QY 220 CysIleGluIleLeuAlaAlaGluProSerThrIleCySAlaGlyLueSerPheGlnVal 239
DB 1051 -----ATCTTTCATTTGAAGAAACCAATCAAGCTCAAGTAGTTCCTTCAGAC 1101
QY 240 ValValArgGlyAsnGlyPheArgHsAlaArxAsnValAsp 253
DB 1102 GAGATGTCAAGAAAGTTCAGCTCAGCTCTCTCAATGAT 1143
RESULT 9
US-09-193-043-45
Sequence 45, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395e1 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45
LENGTH: 3519
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(3516)
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-193-043-45
Alignment Scores:
Pred. No.: 1,296-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 9.61% Indels: 30
DB: 3 Gaps: 12

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US-09-970-076-8 (1-333) x US-09-193-043-45 (1-3519)
Qy 37 ProAlaCysTyrGly---GlyPheAspLeuTyrPheIleuAspLysSerGlySerVal 55
Db 481 CCAAGGTTCAGAGCAAGAGATGAGCATGCTTTCCTGATGATGAGCTCCGGCAGCATT 540
Qy 56 ---LeuHisIstPAsnGluIleTyrTyrPheValGluGlnIleuAlaHisLysPheIle 74
Db 541 GATCAAAAGTGAATTAACCAAGATGAAGACCTTCGCAAGCTTGTATGGGCGAGTTGGCG 600
Qy 75 SerProGlnIleuArgMetSerPheIleValPheSerThrArgGlyThrThleuMetLys 94
Db 601 AGCACCAGACACCTGCTCTCCCTGATGCATACTCAACATCTGTAAAGCTCATTTTACC 660
Qy 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGlnIleu 109
Db 661 TTCACGAAATTCACAGACAGACCTGAGCCCTCAGACCTGTGGATGCCATGCTCCAGCTC 720
Qy 110 GlnLysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgLysSerGlu 129
Db 721 CAA-----GGCCTGACGTACACAGCTCGGGCATCCAGAAAGTGGTGAA 765
Qy 130 GlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeu 148
Db 766 GAGCTATTTCATAGCAGAGATGGGGCCCGAAAGATCCCAAGAAATCTAATTGTCTATC 825
Qy 149 ThrArgGlyGluLeuHisGluAspLeuPheThrPheTyrSerGlu-----ArgGluAlaAsn 166
Db 826 ACAGATGGGCAAAATTCAAGAACCCCTGAGATATGACATGTCATCCCTGAAGCGAG 885
Qy 167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu 185
Db 886 AAAGCT-----GGATCATTTGCGTATGCTATAGGGGTGGAGATGCTTCGGGAA 936
Qy 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199
Db 937 CCCACTGCCCTACAGAGACCTGAACACCATTTGGCTCAGCTCCCTGCAGAACACAGTGTTC 996
Qy 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 219
Db 997 AAGGTGGCAAT---TTGTAGCACTTCGACAGATCCAGCGCAAAATTCAGAGAAA--- 1050
Qy 220 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 239
Db 1051 -----ATCTTGGCATTTGAAGAACCGAATCAAGSTCAAGTAGTCTTTCAGAC 1101
Qy 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253
Db 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 10
US-09-688-307A-45
; Sequence 45, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6432404e1 Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363

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; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

Alignment Scores:
Pred. No.: 1,29e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conserved: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 9.61% Indels: 30
DB: Gaps: 12

US-09-970-076-8 (1-333) x US-09-688-307A-45 (1-3519)
Qy 37 ProAlaCysTyrGly---GlyPheAspLeuTyrPheIleuAspLysSerGlySerVal 55
Db 481 CCAAGGTTCAGAGCAAGAGATGAGCATGCTTTCCTGATGATGAGCTCCGGCAGCATT 540
Qy 56 ---LeuHisIstPAsnGluIleTyrTyrPheValGluGlnIleuAlaHisLysPheIle 74
Db 541 GATCAAAAGTGAATTAACCAAGATGAAGACCTTCGCAAGCTTGTATGGGCGAGTTGGCG 600
Qy 75 SerProGlnIleuArgMetSerPheIleValPheSerThrArgGlyThrThleuMetLys 94
Db 601 AGCACCAGACACCTGCTCTCCCTGATGCATACTCAACATCTGTAAAGCTCATTTTACC 660
Qy 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGlnIleu 109
Db 661 TTCACGAAATTCACAGACAGACCTGAGCCCTCAGACCTGTGGATGCCATGCTCCAGCTC 720
Qy 110 GlnLysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgLysSerGlu 129
Db 721 CAA-----GGCCTGACGTACACAGCTCGGGCATCCAGAAAGTGGTGAA 765
Qy 149 ThrArgGlyGluLeuHisGluAspLeuPheThrPheTyrSerGlu-----ArgGluAlaAsn 166
Db 826 ACAGATGGGCAAAATTCAAGAACCCCTGAGATATGACATGTCATCCCTGAAGCGAG 885
Qy 167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu 185
Db 886 AAAGCT-----GGATCATTTGCGTATGCTATAGGGGTGGAGATGCTTCGGGAA 936
Qy 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199
Db 937 CCCACTGCCCTACAGAGCTGAACACCATTTGGCTCAGCTCCCTGCAGAACACAGTGTTC 996
Qy 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 219
Db 997 AAGGTGGCAAT---TTGTAGCACTTCGACAGATCCAGCGCAAAATTCAGAGAAA--- 1050
Qy 220 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 239
Db 1051 -----ATCTTGGCATTTGAAGAACCGAATCAAGSTCAAGTAGTCTTTCAGAC 1101
Qy 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253
Db 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 11
US-09-350-259-45

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Db      835 AAAGCT-----GGGATCATGCTATAGGGGTGGAGATGCCCTCCGGAA 885
Qy      186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLeuAspHisValPhe 199
Db      886 CCCACTGCCCTACAGAGCTGAACACCATGGCTCAGCTCCCTCCAGAGACCACTGTTTC 945
Qy      200 ProValaAspArgIlePheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValysSer 219
Db      946 AAGGTGGGCAT---TTTGTAAGCACTTCGACAGATCCAGCGCAATTCAGAGAAA--- 999
Qy      220 CysIleGlnIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 239
Db      1000 -----ATCTTGCCATTGAAGAACCGAATCAAGGTCAAGTAAGTTCTTCAGCAGC 1050
Qy      240 ValValaArgGlyAaGlyPheArgHisAlaIaArgaenValaAsp 253
Db      1051 GAGATGTCACAAAGAGTTTCAGCTCAGCTCTCTCAATGAT 1092

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RESULT 14

US-08-605-672-52

Sequence 52, Application US/08605672

Patent No. 5817515

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vlieten, Monica

TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum

STREET: 233 South Wacker Drive, 6300 Seer Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/605,672

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32684

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 3803 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3486

US-08-605-672-52

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Alignment Scores:
Pred. No.: 1.47e-10 Length: 3803
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 9.61% Indels: 30
Gaps: 12

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US-09-970-076-8 (1-333) x US-08-605-672-52 (1-3803)

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Qy      37 ProAlaCysTyrgly---GlyPheAspLeuThrPheIleLeuAspLysSerGlySerVal 55
Db      430 CCAGAGTGTCCAGGACAGAGATGAGCATTTCTTCTTGATGATGAGCTCCGGCGAGCAT 489
Qy      56 ---LeuHisThrPasnGlnIleTyrrTyrrPheValGluGlnLeuAlaHisIlybPheIle 74
Db      490 GATCAAAAGTCACTTAAACCAATGAAGAGCTTCGCAAGCTTTGATGGCCAGTTGGCG 549
Qy      75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
Db      550 AGCAGCAGACACCTGTTCTCCCTGATGCAATATCAATCAATCCGTAAGACTATTTCAC 609
Qy      95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 109
Db      610 TTCAAGGAAATTCAGAGACAGACCTGAGCCCTGAGAGCTGGTGGATGCCATGTCAGCTC 669
Qy      110 GlnIlyValLeuProGlyGlyAspThrTyrrMetHisGluGlnIlePheGluArgAlaSerGlu 129
Db      670 CAA-----GGCCTGACGTACACAGCTTCGGGATCCCAAAAGTGGTGA 714
Qy      130 GlnIleTyrrGluAsnArgGlnGlyTyrrArgThrAla---SerValIleIleAlaLeu 148
Db      715 GAGCTATTTCATAGCAAGAAATGGGCGGCAAAAGTGCAGAAAGATCTAATTGTCTATC 774
Qy      149 ThrAspGlyGluLeuHisGluAspLeuPheThrSerGlu---ArgGlnAlaAsn 166
Db      775 ACAAGTGGGCAAAATTCAGAGACCCCTGAGATAGATACATGTCATCCCTGAAGACAG 834
Qy      167 ArgSerArgAspLeuGlyAlaIleValTyrrCysValGlyValLysAsp---PheAsnIly 185
Db      835 AAAGCT-----GGGATCATGCTATAGGGGTGGAGATGCCCTCCGGAA 885
Qy      186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLeuAspHisValPhe 199
Db      886 CCCACTGCCCTACAGAGCTGAACACCATGGCTCAGCTCCCTCCAGAGACCACTGTTTC 945
Qy      200 ProValaAspArgIlePheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValysSer 219
Db      946 AAGGTGGGCAT---TTTGTAAGCACTTCGACAGATCCAGCGCAATTCAGAGAAA--- 999
Qy      220 CysIleGlnIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 239
Db      1000 -----ATCTTGCCATTGAAGAACCGAATCAAGGTCAAGTAAGTTCTTCAGCAGC 1050
Qy      240 ValValaArgGlyAaGlyPheArgHisAlaIaArgaenValaAsp 253
Db      1051 GAGATGTCACAAAGAGTTTCAGCTCAGCTCTCTCAATGAT 1092

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RESULT 15
US-08-482-293A-52
Sequence 52, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States

ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,293A
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/173,497
 FILING DATE: 23-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,889
 FILING DATE: 5-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/362,652
 FILING DATE: 21-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: William J., Joseph A.
 REGISTRATION NUMBER: 38,659
 REFERENCE/DOCKET NUMBER: 27866/32684
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3803 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3486
 US-08-482-293A-52

Alignment Scores:
 Pred. No.: 1.47e-10 Length: 3803
 Score: 166.00 Matches: 66
 Percent Similarity: 46.15% Conservative: 42
 Best Local Similarity: 28.21% Mismatches: 96
 Query Match: 9.61% Indels: 30
 DB: 2 Gaps: 12

US-09-970-076-8 (1-333) x US-08-482-293A-52 (1-3803)

Qy 37 ProAlaCybTyrgLy---GlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerVal 55
 Db 430 CCAGAGTGTCCAGAGCAAGATGACATGCTTCCGATGATGCGTCCGGCAGCAT 489
 Qy 56 ---LeuHisIstPheGlnIleTyrrTyrrPheValGlnIleuAlaHisLysPheIle 74
 Db 490 GATCAAGTGAATTACCCGATGAGGAGCTTCGTCAGAAAGCTTGATGGCCAGTTGGCG 549
 Qy 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
 Db 550 AGCACCCAGCACCTGCTTCCCTGATGCATATCTCAACATCTGAGAGCTCATTTTACC 609
 Qy 95 LeuThrGlnAspArg-----GlnGlnIleArgGlnGlyLeuGlnGluLeu 109
 Db 610 TTCACGGATTCAGAGCAGCTGAGCCCTCAGAGCCGTGGATGCCATGCTCAGCTC 669
 Qy 110 GlnLysValLeuProGlyGlyAspThrTyrrMetHisGlnGlyPheGlnArgAlaSerGlu 129
 Db 670 CAA-----GGCCTGACATACAGCCTCGGCAATCCAGAAAGTGTGAA 714
 Qy 130 GlnIleTyrrGlnAspArgGlnGlyTyrrArgThrAla---SerValIleIleAlaLeu 148
 Db 715 GAGCATTTCAACAGAAATGGGGCCGCAAAAGTCCAAAGATATCTAATTGTCTATC 774

Qy 149 ThrAspGlyGluLeuHisGlnAspLeuPhePheTyrrSerGlu-----ArgGlnAlaAsn 166
 Db 775 ACAGATGGCAGAAATTACAGAGACCCCTGGAGTATGACATGTCATCCCTGAAAGCAGAG 834
 Qy 167 ArgSerArgAspLeuGlyAlaIleValTyrrCysValGlyValLysAsp---PheAsnGlu 185
 Db 835 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCCCTTCCGGGAA 885
 Qy 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199
 Db 886 CCCACTGCCCTTACAGAGCTGAACACCATTTGGCTCAGCTCCCTGCGAGACACGTGTTCC 945
 Qy 200 ProValAspAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 219
 Db 946 AAGTGGGCAAT---TTTGACACCTTCGACATCCAGCGGCAAAATTCAGAGAAA--- 999
 Qy 220 CysIleGlnIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 239
 Db 1000 -----ATCTTGGCATTTGAAGGAAACCAATCAAGGTCAGATGTTCTTTCACAGCAC 1050
 Qy 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253
 Db 1051 GAGATGTCAACAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1092

Search completed: June 22, 2004, 02:55:01
 Job time : 87.528 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	1650	54.5	2459	4	US-09-833-381-998	Sequence 998, App1
2	1392	46.0	1609	4	US-09-620-312D-8	Sequence 8, App1
3	213	7.0	318	3	US-09-165-264-12	Sequence 12, App1
4	213	7.0	320	3	US-09-165-264-14	Sequence 14, App1
5	208	6.9	320	3	US-09-165-264-13	Sequence 13, App1
6	206	6.8	320	3	US-09-165-264-7	Sequence 7, App1
7	205.5	6.8	51259	3	US-08-781-891-209	Sequence 209, App1
8	205.5	6.8	51259	4	US-09-618-166-109	Sequence 109, App1
9	205	6.8	320	3	US-09-165-264-11	Sequence 11, App1
10	203	6.7	319	3	US-09-165-264-8	Sequence 8, App1
11	199.5	6.6	324	4	US-08-547-653-234	Sequence 234, App1
12	199	6.6	53577	3	US-08-654-116-1	Sequence 1, App1

13	195	6.4	16442	3	US-08-761-691-208	Sequence 208, App
14	195	6.4	16442	4	US-09-618-166-058	Sequence 208, App
15	194	6.4	53526	3	US-08-658-136-2	Sequence 2, Appli
16	192	6.3	43280	2	US-08-804-227C-1	Sequence 1, Appli
17	191.5	6.3	2230	1	US-08-217-327-5	Sequence 5, Appli
18	189.5	6.3	1926	4	US-09-249-885A-2	Sequence 2, Appli
19	189.5	6.3	1926	4	US-09-410-399-3	Sequence 3, Appli
20	189.5	6.3	2580	3	US-09-050-863-2	Sequence 2, Appli
21	189.5	6.3	2580	4	US-09-359-081-2	Sequence 2, Appli
22	189.5	6.3	5452	2	US-09-130-114-1	Sequence 1, Appli
23	189.5	6.3	8705	4	US-09-647-344A-14	Sequence 14, Appli
24	189.5	6.3	9600	3	US-08-910-647-1	Sequence 1, Appli
25	189.5	6.3	9600	4	US-09-620-925-1	Sequence 1, Appli
26	189.5	6.3	10596	4	US-07-884-811-15	Sequence 15, Appli
27	189.5	6.3	10596	1	US-07-885-971-15	Sequence 15, Appli
28	189.5	6.3	10596	1	US-08-087-783A-15	Sequence 15, Appli
29	189.5	6.3	10596	2	US-08-134-088B-15	Sequence 15, Appli
30	189.5	6.3	10596	2	US-08-134-088B-15	Sequence 15, Appli
31	189.5	6.3	10596	5	PCT-US93-04648-15	Sequence 15, Appli
32	189.5	6.3	12001	1	US-08-458-568A-11	Sequence 11, Appli
33	189.5	6.3	16080	4	US-09-724-566A-48	Sequence 48, Appli
34	187.5	6.2	925	3	US-08-858-003-1	Sequence 1, Appli
35	187.5	6.2	925	3	US-09-078-166-1	Sequence 1, Appli
36	187.5	6.2	925	3	US-08-997-467-1	Sequence 1, Appli
37	187	6.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
38	187	6.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
39	186.5	6.2	3196	4	US-09-704-449-1	Sequence 1, Appli
40	186.5	6.2	152331	3	US-09-128-155-16	Sequence 16, Appli
41	186	6.1	246	4	US-09-547-693-332	Sequence 232, App
42	186	6.1	913	1	US-08-217-327-3	Sequence 3, Appli
43	186	6.1	913	1	US-07-885-970A-3	Sequence 3, Appli
44	186	6.1	913	1	US-08-298-687A-3	Sequence 3, Appli
45	186	6.1	913	1	US-08-530-797-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

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US-09-833-381-998
; Sequence 998, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: ROBISON, Keith E.
; TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 998
; LENGTH: 2459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2459)
; OTHER INFORMATION: n = A,T,C or G
; US-09-833-381-998

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Alignment Scores:

Pred. No.:	5,18e-116	Length:	2455
Score:	1650.00	Matches:	361
Percent Similarity:	65.98%	Conservative:	21
Best Local Similarity:	62.33%	Mismatches:	76
Query Match:	54.55%	Indels:	124
DB:	4	Gaps:	12

US-09-970-076-6 (1-564) x US-09-833-381-998 (1-2459)

QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20

Db 412 ATGGCCACGGCGAGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGCCACT 471
Qy LeuValIleuIleCysAlaGlyGlnGlyIleYArgArgIleuAspGlyIleProAlaCysTyr 40
Db 472 CTGGGCTCATCTGGCCGGCGAGGGGAGCCGAGGAGATGGGGGCTCCAGCTGCTAC 531
Qy 41 GlyIlePheAspLeuTyrPheIleuAspIleSerGlySerValIleuIleHisTyrPhe 60
Db 532 GGGCGATTGACCTGTATCTTCATTTTGGACAAATCAGAGAGTGTCTGCACACATGGAAT 591
Qy 61 GluIleTyrTyrPheValGluGlnIleuAlaHisIleYSerPheIleSerProGlyIleuAspMet 80
Db 592 GAAATCTATTAATCTTGTGAAACAGTTGGCTCCCAAAATTCATCAGCCCAAGTGAAGATG 651
Qy 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetIleYSerValIleuThrGluAspArgGlu 100
Db 652 TCCTTATTTGTTTCTCCACCGAGGAACACTTAAGAACTGACAGAAACAGAGAA 711
Qy 101 GlnIleArgGlnGlyLeuGlnGlnIleuGlnIleuValIleuProGlyIleYAspThrTyrMet 120
Db 712 CAAATCCCTCAAGGCTGAGAAAGAACTCCAGAAAGTTTGCAGAGAGAGACACTTACATG 771
Qy 121 HisGlnGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAspArgGlnGlyTyrArg 140
Db 772 CATGAAGATTGAAAGGGCCAGTGAAGAGATTATTAAGAAACAGCAAGGGTACAG 831
Qy 141 ThrAlaSerValIleIleAlaIleuThrAspGlyGlnIleuHisGluAspLeuPheTyr 160
Db 832 ACAGCAGCCTCATATTCCTTGAATGAGAACTCCATGAAGATCTTTTTCAT 891
Qy 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db 892 TCAGAGAGGAGGCTAATAGTCTGAGATCTTGGTCAATGTTACTGTGTGGTGTG 951
Qy 181 LysAspPheAsnGluThrGlnIleuAlaArgIleAlaAspSerIleAspHisValPhePro 200
Db 952 AAAGATTTCATGAACACAGCTGGCCCGAGATGGGAGAGAGATCATGTGTTCC 1011
Qy 201 ValAsnAspGlyPheGlnAlaIleuGlnGlyIleIleHisSerIleLeuIleYSerCys 220
Db 1012 GTGAATGACGGCTTCAAGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCCGCG 1071
Qy 221 IleGlnIleuAlaIleGluProSerThrIleCysAlaGlyIleuSerPheGlnValVal 240
Db 1072 ATCGAAATTTCAAGCAGTGAACCATCCACATATGTGAGAGAGTCAATTCAGATTGTC 1131
Qy 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValaAspArgValIleuCysSerPheIle 260
Db 1132 GTGAGAGGAAACGGCTTCCGACATGCCGCAACGTCGACAGGGTCTCTGACAGCTTCAG 1191
Qy 261 IleAsnAspSerValThrLeuAsnGluYSerProPheSerValGluAspThrTyrLeuIleu 280
Db 1192 ATCAATGATCGGTGACACTCATAGAAAGCCCTTTCTGTGGAAGATCTTATTACTG 1251
Qy 281 CysProAlaProIleLeuIleGlyValaIleYMetIleValaIleuGlnValSerMetAsn 300
Db 1252 TGTCCAGCGCTATCTTAAAGAGTGTGCATGAAGCTGCACCTCAGTCAAGCATGAAC 1311
Qy 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrHisCysSerAspGly 320
Db 1312 GATGGCTCTCTTTATCTCAGTTCATCATCACACACACACTGTAGCTTCAC 1371
Qy 321 SerIleLeuAlaIleAlaIleuIleuPheLeuIleuAlaIleuAlaIleuIleuTrp 340
Db 1372 AAAATTGCATCA----- 1383
Qy 341 TrpPheTrpProLeuCysCysThrValIleIle---IleGluValProProProProAla 359
Db 1384 -----GGCCCAACAAGCTGCTTGATGGAATGACAGAAATACCCGCTGCTCCCTCC 1437
Qy 360 GluGluSerGluGlnGluAspAspAspGlyLeuProIleYIleYTrpProThrValaAsp 379
Db 1438 GGACAGCACTCTGTAAGAAC----- 1458

Qy 380 AlaSerTyrTyrGlyIleArgGlyValGlyIleYIleYAspArgMetGluValArgTrpGly 399
Db 1459 -----GGG 1461
Qy 400 GluIleYSerThrGluGlnGlyAlaIleuGlnIleuValaIleYAsnAlaArgValIle 419
Db 1462 GAGAGAGGA-----GCCAAACATGCTCGGTTTACA 1491
Qy 420 Met-----ProGluGlnIleuYTrpIlePheProGlu 429
Db 1492 CTTTCTTATTTACTGATGATGAGGAGGAGAGACAGGCTGGAGTTAGCACACTGAG 1551
Qy 430 ProArgAsnLeuAsnAsnMetLeuArgArgProSerSerProArgIleYTrpTyrSerPro 449
Db 1552 TGCCCCAACAATGGAAGAAACATCAGAGG-----GACAGGAAGC-TTCCCTCCT 1601
Qy 450 -----IleYIleYIleYLeuAspAlaIleuTrpValIleu-----Leu 461
Db 1602 TAAACCAAGTTTTCAGACTTACTGAGGACCTTATTTGGGCTTACATTAATCACTCCATG 1661
Qy 462 ArgIleYIleYAspArgValSerValMetArgProGlnProGly-----AspThr 478
Db 1662 CGGTGGCATCAGGACAAATCTGCTGACAGACCCAACTTGAAGTGAAGATTTCAACAGT 1721
Qy 479 GlyArgCysIleAsnPheThrArgValIleAsnAsnGlnProAlaIleYTrpProLeuAsn 498
Db 1722 TTTCTTATTTTGAATCTCCCGCAGGCTCCACATTAATCTCTCATTTCTAT----- 1772
Qy 499 AsnAlaIleHisThrSerSerProProProAlaProIle----- 511
Db 1773 -----CTCTCTCTCTTCCCAAAAGAAAAGAGAGAGCAG 1811
Qy 512 -----TyrThrPro 514
Db 1812 CAGTGTGATACCGTATCATCCAGAGGCTGTTCTCTCCATTATAGGCAAAACAAGC 1871
Qy 515 ProProProAlaProHisCysProProProPro-----ProSerAlaProThr 530
Db 1872 CCGTGAAGAATATTCTACTCCCGCCCATGCGATTAATAATCAAAATTCCTATATA 1931
Qy 531 ProProIleProSer 535
Db 1932 TTCACCTGCCAAGC 1946

RESULT 2
US-09-620-312D-8
Sequence 8, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jians-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungding
APPLICANT: Wang, Zhimei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: Polypeptides
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 8
LENGTH: 1609
TYPE: DNA
ORGANISM: Homo sapiens.
FEATURE:
NAME/KEY: CDS
LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 1,12e-96 Length: 1609
Score: 1392.00 Matches: 267
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.26% Mismatches: 0
Query Match: 46.02% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-6 (1-564) x US-09-620-312D-8 (1-1609)

QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 309 ATGGCCAGCGCGGAGCGAGAGCCCTCGGCATCGCTTCCATGCTCTCTTGGCCACT 368

QY 21 LeuValLeuIleCysAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTyr 40
DB 369 CTGGGCTCATCTGCGCGCGGAGCGGAGCGGAGGAGATGGGGGCTCAGCCGTAC 428

QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspGlySerGlySerValLeuHisIleTrpAsn 60
DB 429 GCGCGATTGACCTGACTTCACTTTTGACAAATCAGGAAGTGTCTGCACACCTGAAAT 488

QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIleValPheIleSerProGlnLeuArgMet 80
DB 489 GAAATCTATTACTTGTGGACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 548

QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetIleLeuThrGluAspArgGlu 100
DB 549 TCTCTTATTGTTTCTTCCACCGGAGAAACAACCTTAATAAATGACAGAAACAGAGA 608

QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnIleValLeuProGlyAspThrTyrMet 120
DB 609 CAAATCCGTCAGAGCGCTAGAGAACTCCAGAAATGTTCTGCCAGAGAGACCTTAACATG 668

QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAspArgGlnIleTyrArg 140
DB 669 CATGAAGGATTGAAAGGCGCAGTGCAGATTATATGAAACAGACAGAGGTAACAG 728

QY 141 ThrAlaSerValIleIleIleLeuThrAspGlyGluLeuHisIleValLeuAspLeuPheTyr 160
DB 729 ACAGCAGAGGTATCATCTTCTTGAATGAGAACTCAGAAATGATCTCTTTTTCAT 788

QY 161 SerGluArgGluAlaAspAspSerArgAspLeuGlyAlaIleValIleTyrCysValGlyVal 180
DB 789 TCAGAGAGGAGGAGCTAAATGCTGTGAGATCTTGGGCAATGTTTACTGTGTGTGG 848

QY 181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerIleAspHisIleValPhePro 200
DB 849 AAAGATTTCATAGACACAGCTGGCCGATGGCGAGACAGTAAGATCATGTGTTCC 908

QY 201 ValAspAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleLysSerCys 220
DB 909 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCAATTTTGAAGAAGTCCTGC 968

QY 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
DB 969 ATCGAAATTTCTAGCAGCTGACCATCCACATATGTCGAGAGAGATTCATTAAGTTGTC 1028

QY 241 ValArgGlyAsnGlyPheArgHisAlaIleAsnValAspArgValLeuCysSerPheLys 260

DB 1029 GTGAGAGAAACGGCTTCGACATGCGCGCAACGTGACAGGCTCTGCGAGTTCAAG 1088

QY 261 IleAsnAspSerValThrLeuAsnGlu 269
DB 1089 ATCAATGACTCGTCCACACTCAGTAAG 1115

RESULT 3
US-09-165-264-12/C
Sequence 12, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamorthy, Thuralayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1996-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 318
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-12

Alignment Scores:
Pred. No.: 4.04e-08 Length: 318
Score: 213.00 Matches: 36
Percent Similarity: 60.66% Conservative: 1
Best Local Similarity: 59.02% Mismatches: 24
Query Match: 7.04% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-6 (1-564) x US-09-165-264-12 (1-318)

QY 502 HisThrSerSerProProAlaProIleTyrThrProProProAlaProHisCys 521
DB 310 CACACACACACCC 251

QY 522 ProProProProSerAlaProThrProProIleProSerProProSerThrLeuPro 541
DB 250 CC 191

QY 542 ProProProGlnAlaProProProAsnArgAlaProProProSerArgProProArg 561
DB 190 CC 131

QY 562 Pro 562
DB 130 CCC 128

RESULT 4
US-09-165-264-14/C
Sequence 14, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamorthy, Thuralayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1996-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-14

Alignment Scores:	
Pred. No.:	4.07e-08
Score:	213.00
Best Similarity:	59.68%
Best Local Similarity:	58.06%
Query Match:	7.04%
DB:	3
	Gaps: 0
	Indels: 0
	Mismatches: 25
	Conservative: 36
	Matches: 32
	Length: 32

Oy	521	CysProBProBProProSerAlaProThrProFolioProSerProSerThrLeu	540
Db	307	TGGACACC	248
Oy	501	TyrHisHiseSerProProFoliaProIleYthrProBProBAlaPhe	520
Db	307	TGGACACC	248
Oy	541	ProBProBProGlnAlaProProProAlaArgAlaProProProSerArgProPro	560
Db	187	CCC	128
Oy	561	ArgPro	562
Db	127	CCCCCC	122

```

RESULT 5
US-09-165-264-13/c
; Sequence 13. Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vineyagamoorthy, Thuraiyah
; TITLE OF INVENTION: Multi-Loct Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ. ID NOS.: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer sequences
US-09-165-264-13

```

Alignment Scores:	
Pred. No.:	9.77e-08
Score:	208.00
Percent Similarity:	60.00%
Best Local Similarity:	60.00%
Query Match:	6.86%
DB:	3
Length:	320
Matches:	36
Conservative:	0
Mismatches:	24
Indels:	0
Gaps:	0

[illegible]

RESULT 6
US-09-165-264-7/c
; Sequence 7, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:

```

: APPLICANT: Vinayagamoorthy, Thruthalayah
: TITLE OF INVENTION: Multi-Loci Genomic Analysis
: FILE REFERENCE: 44747
: CURRENT APPLICATION NUMBER: US/09/165,264
: CURRENT FILING DATE: 1998-10-01
: NUMBER OF SEQ. ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.1
: SEQ. ID NO. 7
: LENGTH: 320
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
US-09-165-264-7

```

Alignment Scores:	
Pred. No.:	1.39e-07
Score:	206.00
Percent Similarity:	58.73%
Best Local Similarity:	57.14%
Query Match:	6.81%
DB:	3
Length:	32
Matches:	36
Conservative:	1
Mismatches:	26
Indels:	0
Gaps:	0

QY	500	AlaTyrHisIhmSerSerProProAlaProIleTyrTrpProProAlaPro	518
		::	
Db	313	GCAAGGTAAGCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	25
QY	520	HisCysProProProProSerAlaProThrProProlleProSerProSerThr	539
Db	253	CC	194
QY	540	LeuProProProGlnAlaProProProAlaGlnAlaProProProSerArgProPro	555
Db	193	CC	134
QY	560	ProArgPro	562
Db	133	CCCCCCCC	125

RESULT 7
 US-08-781-891-209
 : Sequence 209, Application US/08781891
 : Patent No. 6090620
 : GENERAL INFORMATION:
 : APPLICANT: Fu, Ying-Thi
 : APPLICANT: Yu, Chang-Shi
 : APPLICANT: Oshima, Junko
 : APPLICANT: Mulligan, John T.
 : APPLICANT: Schellenberg, Gerald D.
 : TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
 : TITLE OF INVENTION: WERNER'S SYNDROME
 : NUMBER OF SEQUENCES: 209
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SEED and BERRY LLP
 : STREET: 6300 Columbia Center, 701 Fifth Avenue
 : CITY: Seattle
 : STATE: Washington
 : COUNTRY: USA
 : ZIP: 98104-7092
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC Compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent/US Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/781,891
 : FILING DATE: 27-DEC-1996
 : CLASSIFICATION: 800
 : ATTORNEY/AGENT INFORMATION:
 : NAME: No. 6030620Leuburg Ph.D., Carol
 : REGISTRATION NUMBER: 39,317

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 209:
US-09-618-166-209

Alignment Scores:
Pred. No.: 0.000168 Length: 51259
Score: 205.50 Matches: 37
Percent Similarity: 70.18% Conservative: 3
Best Local Similarity: 64.91% Mismatches: 12
Query Match: 6.79% Indels: 5
DB: 4 Gaps: 2

US-09-970-076-6 (1-564) x US-09-618-166-209 (1-51259)
Qy 506 ProProProAlaProIleYrThrProProProProAlaProHISyProProProPro 523
Db 46 CttCttCttGttCttGttCttGttCttGttCttGttCttGttCttGttCttGttCtt 99

Qy 526 ProSerAlaProThrProProIleProSerProProSerThrLeuProProProGln 545
Db 100 CttGcccccCttCttCttCttCttCttCttCttCttCttCttCttCttCttCttCtt 150

Qy 546 AlaProProProAlaGlnAlaProProProSerArgProProProArgPro 562
Db 151 GcttCttCttCttCttCttCttCttCttCttCttCttCttCttCttCttCttCttCtt 201

RESULT 9
US-09-165-264-11/c
; Sequence 11, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamoorthy, Thuraiyiah
; TITLE OF INVENTION: Multi-Loci Genomic Analyses
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-11

Alignment Scores:
Pred. No.: 1.65e-07 Length: 320
Score: 205.00 Matches: 35
Percent Similarity: 61.02% Conservative: 1
Best Local Similarity: 59.32% Mismatches: 23
Query Match: 6.78% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-6 (1-564) x US-09-165-264-11 (1-320)
Qy 504 SerSerProProProAlaProIleYrThrProProProProAlaProHISyProPro 523
Db 305 TctGtccccccccccccccccccccccccccccccccccccccccccccccccccc 248

Qy 524 ProProProSerAlaProThrProProIleProSerProProSerThrLeuProProPro 543
Db 245 Cttccccccccccccccccccccccccccccccccccccccccccccccccccc 166

Qy 544 ProGlnAlaProProProAlaGlnAlaProProProSerArgProProProArgPro 562
Db 185 Cttccccccccccccccccccccccccccccccccccccccccccccccc 129

RESULT 10
US-09-165-264-8/c
; Sequence 8, Application US/09165264

```

Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuralayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 8
LENGTH: 319
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
US-09-165-264-8

Alignment Scores:
Pred. No.: 2,33e-07 Length: 319
Score: 203.00 Matches: 35
Percent Similarity: 58.33% Conservative: 0
Best Local Similarity: 58.33% Mismatches: 25
Query Match: 6.71% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-6 (1-564) x US-09-165-264-8 (1-319)

Qy 503 ThrsrserProProProAlaProIleTyThrProProProProAlaProHisCysePro 522
Db 301 ACCC 242
Qy 523 ProProProProSerAlaProThrProProIleProSerProProSerThrlauProPro 542
Db 241 CC 182
Qy 543 ProProGlnAlaProProProGlnAlaProProProProSerArgProProProArgPro 562
Db 181 CC 122

RESULT 11
US-09-547-693-234
Sequence 234, Application US/09547693
Patent No. 6639050
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: PatentIn version 3.0
SEQ ID NO 234
LENGTH: 324
TYPE: DNA
ORGANISM: Artificial/Unknown
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Synthetic
US-09-547-693-234

Alignment Scores:
Pred. No.: 4,39e-07 Length: 324
Score: 199.50 Matches: 43
Percent Similarity: 54.26% Conservative: 8
Best Local Similarity: 45.74% Mismatches: 38
Query Match: 6.60% Indels: 5
DB: 4 Gaps: 2

US-09-970-076-6 (1-564) x US-09-547-693-234 (1-324)

Qy 473 ProGlnProGlyAsp-ThrGlyArgCysIleAsnProThrArgValTysAsnAsnGlnPr 492
|||||
|||

Db 5 CCTCAACCCGGGCGCTCCACCAACCACTTCACCTCCACCCCATCTCCACCAACCACTT 64
Qy 492 oAlaLeTy-ProleuAsnAsnAlaTyH1sThrSerSer-ProProProAlaProIleT 512
Db 65 CACCTCACCCCATCTCCACCAACCACTTCACCTCCACCCCATCTCCACCAACCA---C 121
Qy 512 yThrProProProProAlaProHisCyseProProProProSerAlaProThrProP 532
Db 122 CTTCACCTCCACCCCATCTCCACCAACCACTTCACCTCCACCCCATCTCCACCAAC 181
Qy 532 roIleProSerProProSerThrlauPro-----ProProGlnAlaProProProA 550
Db 182 CTTCACCTCCACCCCATCTCCACCAACCACTTCACCTCCACCCCATCTCCACCAAC 241
Qy 550 snArgAlaProProProSerArgProProProArgPro 562
Db 242 CTTCACCTCCACCCCATCTCCACCAACCACTTCACCTTCACCT 279

RESULT 12
US-08-658-136-1
Sequence 1, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Alignment Scores:
Pred. No.: 0.000556 Length: 53577
Score: 199.00 Matches: 91
Percent Similarity: 32.35% Conservative: 29
Best Local Similarity: 24.53% Mismatches: 124
Query Match: 6.58% Indels: 128
DB: 3 Gaps: 16

US-09-970-076-6 (1-564) x US-08-658-136-1 (1-53577)


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US-08-658-136-2
: Sequence 2, Application US/08658136
: Patent No. 6071717
: GENERAL INFORMATION:
: APPLICANT: KLINGER, KATHERINE W
: APPLICANT: LANDES, GREGORY M
: APPLICANT: BURN, TIMOTHY C
: APPLICANT: CONNORS, TIMOTHY D
: APPLICANT: DACKOWSKI, WILLIAM
: APPLICANT: GERRINO, GREGORY
: APPLICANT: QIAN, PENG
: TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
: NUMBER OF SEQUENCES: 58
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: GENZYME CORPORATION
: STREET: ONE MOUNTAIN ROAD
: CITY: FRAMINGHAM
: STATE: MASSACHUSETTS
: COUNTRY: USA
: ZIP: 01701
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/658,136
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: LASSEN, ELIZABETH
: REGISTRATION NUMBER: 31,845
: REFERENCE/DOCKET NUMBER: GENA-17.8
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 508-872-8400
: TELEFAX: 508-872-5415
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 53526 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Alignment Scores:
Pred. No.:
Score: 0.00133 Length: 53526
Percent Similarity: 194.00 Matches: 92
Best Local Similarity: 32.53% Conservative: 29
Query Match: 24.73% Mismatches: 123
6.41% Indels: 129
3 Gaps: 16

US-09-970-076-6 (1-564) x US-08-658-136-2 (1-53526)
QY 271 ProPheserValgluAphrThrTLeuLeuCyPProAlaProIleLeuYsgluValGly 290
Db 33755 CCGGCCCTCCGCGCTGTCAGACTGCTGTGCCCTCCCTCCGAGCCAGTACGCAAGNA 33814
QY 291 -MetLyAlAlA-----LengInValSerMetAs 300
Db 33815 CCTGGACGTGGCGGCGAGCGCCAGACAGACGCGGCGACCGAGCCCAATACGCAAGNA 33874
QY 300 nAspGlyLeuSerPheIleSerSerSerValIleIleIleThrThrThrHisCySerAspG1 320
Db 33875 C-----ATCAGCGAGACTCGTGTGCTCCCGAGGGGTCCACACGTGGATGA 33919
QY 320 ySerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTr 340
Db 33920 C-----ATCAGAGAGATCGCTGCTGCTGCTGCGCTGCGCCAGTGCAT 33955
QY 340 pTrpPheTrpProLeuCySerThrValIleIleYsgluValProProProAlaG1 360
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Db 33956 GGTAGATGCCCCACCTGCTAC-----CTGCCCGCATGCTGCAG 34000
Qy 360 uGluSerGluGluGluAspAspAspGlyLeuProGlyLysTrpProThrValAspAl 380
Db 34001 GGCACTGGGTTCAAGCCCCAGGGC-----AGACGGGACGCTGGCCAGAGACTGAGC 34054
Qy 380 aSerTyTyrgly----- 384
Db 34055 CTCAGACCTGGCTCTCTCTCCATGAGGTTCTCGGTCTGACCTGCTTCAATGAGCC 34114
Qy 385 -----GlyArgGlyValGlyLysLeuAsp 393
Db 34115 TCAGCCGTTCTGCTCTGTGTAAAGAGAGTGTCTCGGGGAGCCAGGAGGTGTAAAGAG 34174
Qy 393 gMeGluValArgTrpGlyGluLysGlySerThrGluGluGlyAlaLysLeuGluLysAl 413
Db 34175 G-----GCCCAAGTGT-GGGAGAGGACTAAGAGATG 34206
Qy 413 aLysAsnAlaArgValLysMetProGluGluGluTrpGluPheProGluProArgAsnLe 433
Db 34207 CTGCTGTGCTCCCTCCACTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT----- 34258
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Qy 453 aLeuAspAlaLeuTrpValLeuLeuArgLysGlyTyraArgValSerValMetArgPr 473
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Db 34330 CCAGCCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTTC 34389
Qy 493 aLysTyTrpProLeuAsnAsnAlaTy-----HisThrse 504
Db 34390 CCTCTCTCTCTCCCTAGACCTTCCCTCACCTCTCTCCGCTGAGCCCTCCACTCGTC 34449
Qy 504 r-----SerPr 506
Db 34450 CCCCAGCCCTCCCTCCCTAGCCCTCCCTCCCTCTCTCCCTCTCCCTCCCTCCCTCC 34509
Qy 506 oProProAlaProIleTyTrhProProBro-----ProAl 518
Db 34510 TCCTCCCTCCCTCTCTCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 34569
Qy 518 aProHisCysProPro-----ProProProSerAlaProThrProProIleProSerPr 536
Db 34570 CCCCTCTCTCTCCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 34629
Qy 536 oProSerThrLeuProProProProGluAlaProProProAsnArgAlaProPro----- 554
Db 34630 CTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 34683
Qy 555 ----ProSerArgProProProProArgProSerVal 564
Db 34684 CCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 34717
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